```
gb_pat:AX335777
gb_pat:AX336076
gb_pat:AX336340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ch information block:
Query: US-10-040-803-7
Query length: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: Aug 13, 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_pr:AB010779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search time (sec): 1864.040000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database sequences: 1797656
Database length: 1873333701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_pat:AX342626
gb_ro:AF188613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_ro:RRA5642
                                                                                                                                          gb_ro:MUSPROT6B
gb_pat:AX342632
                                                                                                                                                                                                                                                                                                                gb_ro:MMU243866
gb_om:OAR18223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MODEL-frame+_p2n.mode1 -DEV=x1h
-Q=/cgn2_1/USPTO_spco1/US10040803/runat_13082002_083352_7339/app_query.fasta_1.378
-Q=/cgn2_1/USPTO_spco1/US10040803/runat_13082002_083352_7339/app_query.fasta_1.378
-Q=-gapexi=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.500
-GAPEXT=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=4.500 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPOP=10.000
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=10 -MODE=LOCAL -OUTFMT=pfs
-NORM-ext -HEAPSIZE=500 -ALIGN=10 -MAXLEN=200000000
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLEXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                       gb_pat:AX207905
                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_pat:AX338508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_ro:AB038244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_ro:BC003851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_ro:AB017638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_pr:BC001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_ro:AF378085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jb_pat:AX098193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of: US-10-040-803-7 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB038496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMPROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Results were produced by the GenCore software, version 4.5, copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strd Orig
+ 1720.00
+ 1720.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1:35 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                           .50
2372.0876
2372.64
2372.64
2372.64
1017.36
11685.32
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
1017.36
101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8e-38
6.8e-38
                                                       8.2e-33
8.2e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9e-36
2.3e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9e-38
                                                                                                                                                                                                                                                                                                                            1.5e-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1e-74
1.6e-48
.5e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.6e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L.6e-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EScore Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4e-124
.5e-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .9e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0e-1
                                                                                                                    .2e-33
                                                                                                                                                                                                       .3e-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                              .4e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0e-38
                                                                                                                                                                                                                                      .2e-34
                                                                                                                                                                                                                                                                  .5e-33
                                                                                                                                                                                                                                                                                             .3e-33
                                                                                                                                                                                                                                                                                                                                                        .2e-34
                                                                                                                                                                                                                                                                                                                                                                                .6e-35
                                                                                                                                                                                                                                                                                                                                                                                                                  .8e-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 I AJ36593 Homo sapiens mRNA for 8 I AB018694 Xenopus laevis Xepsin 6 I AX098193 Sequence 105 from Pet 105 F
                                                                                                                                                                                                                                                     AF202076 Rattus norvegicus pro
AF202076 Rattus norvegicus mRN
AF31824 Ovis aries mRNA for tryp
BC003851 Mus musculus, Similar
AF378085 Mus musculus prostasi
AF378085 Mus musculus mRNA for
AF378265 Sequence 23 from Pata
AF378265 Sequence 27 from Pata
AF188613 Mus musculus channel
AF175522 Homo sapiens transmen
BC010970 Mus musculus, Similar
AF17552 Homo sapiens transmen
BC010970 Mus musculus mRNA for
LY1823 Ovis aries mRNA for try
AX207905 Sequence 9 from Paten
AX207905 Sequence 7 from Paten
LAX207905 Sequence 7 from Paten
LAX207905 Sequence 7 from Paten
LAX207905 Sequence 7 from Paten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB010779 Homo sapiens hBSSP-4
AF321182 Homo sapiens serine p
BC009726 Homo sapiens, proteas
AB010778 Mus musculus mBSSP-4
AJ005642 Rattus rattus mRNA er
AC003965 Homo sapiens chromos
                              M24664 Dog mast cell tryptase i
AR080456 Sequence 4 from patei
D38455 Rat mRNA for mast cell
U67909 Rattus norvegicus mast
                                                                                                                                                   AR080464 Sequence 20 from pate
M57626 Mouse protease-6 gene,
AX342632 Sequence 29 from Pate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB038496
                                                                                                                                                                                                                                         L31853 Mus musculus serine pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis Xesp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_om:AB038652
gb_pat:E21865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr:AB010779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                   alignment_block:
US-10-040-803-7 x AB010779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 5.426
Percent Similarity: 100.000
                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
            54 CTTCACCTCCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCA 10:
                                                                      17
                                                                                                                                 4
                                                                      rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA 34
                                                                                                                                 ATGGTGGTTTCTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease, hBSSP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete cds. AB010779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1720.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (sites)
                                                                                                                                                                                                                                                  to: AB010779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 957
```

```
gb_pat:AX207901
gb_pat:E40571
                        1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyGySLeuGlyTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens hBSSP-4 mRNA for brain-specific serine protease-4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-JAN-1998) Nozomi Yamaguchi, Institute for Geriatrics, Kyoto Prefectural University of Medicine, Department of Cell Biology; Kajii-cho 465, Kamigyo-ku, Kawaramati Hirokoji, Kyoto, Kyoto 602-8566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp, Tel:81-75-251-5848(ex.5848), Fax:81-75-251-5848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens brain cDNA to mRNA. Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1306)
Yamaguchi, N. and Mitsui, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitsui,S., Okui,A., Kominami,K. and Yamaguchi,N. Cloning and characterization of a human brain-specific serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB010779.1 GI:12248750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQ
GPITEDMICAGYLEGERDACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYI
SLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQGSGAAARS"
4 432 c 402 g 253 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="brain-specific serine protease-4"
/product="brain-specific serine protease-4"
/protein_id="BAB20263.1"
/protein_id="BAB20263.1"
/db_xref="G1:12248751"
/db_xref="G1:12248751"
/translation="MYSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKP
/translation="MYSGAPPALGGGCLGTFTSLLLASTAILNAARIPVPPACGKP
/translation="MYSGAPPALGGGCLGTFTSLLLASTAILNAARIPVPPACGKP
/translation="MYSGAPPALGGGCLGTFTSLL"
/translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="brain"
4. .957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="prosemin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="hBSSP-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="hBSSP-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534.00
532.50
532.50
531.50
531.50
                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  736.73
733.31
731.30
730.82
729.72
                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1306 bp
                                                                                                                                                                         to: 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1e-32
1.8e-32
2.3e-32
2.4e-32
2.8e-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | AX207901 Sequence 5 from Pat
| E40571 Novel protease and DN
7 | AB038652 Sus scrofa pMCT7 m
| E21865 Novel acidophil serin
1 | AB031330 Homo sapiens esp-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI 17-MAY-2001
```

```
284
                                                          904
                                                                                     301
                                                                                                                    854
                                                                                                                                                                           804
954 C 954
                           317 r 317
                                                                                                                                                                                                         267
                                                                                                                                                                                                                                    754
                                                                                                                                                                                                                                                                251
                                                                                                                                                                                                                                                                                                                                                   654
                                                                                                                                                                                                                                                                                             704
                                                                                                                                                                                                                                                                                                                                                                                217
                                                                                                                                                                                                                                                                                                                                                                                                             604
                                                                                                                                                                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304
                                                                                                                                                                                                                                                                                                                  :34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                 GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaAlaArgSe 317
                                                     rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly 300
                                                                                                                                                                                     aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT 284
                                                                                                                                                                                                                                                                                                      luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal
                                                                                                            GGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGGGG
                                                                                                                                                                        CGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCGCACCGCTCCT
                                                                                                                                                                                                                                GACGGCGCCTGGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGC
                                                                                                                                                                                                                                             AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl 267
                                                                                                                                                                                                                                                                                                                                                               CCACCTCCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCC
                                                                                                                                                                                                                                                                                       AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                                                                                                                                                                ACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTTGGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                        CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                      ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                              eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerII 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9SerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTTCTCTGTGCTGGGGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpVallleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGGCGGCGAGGACAGCAGCGAGCGAGTGGCCCTGGATCGTGAGCAT
                                                                                                              903
                                                                                                                                                                                                                                803
                                                                                                                                                                                                                                                                                       753
                                                                                                                                                                                                                                                                                                                                                                           234
                                                                                                                                                                                                                                                                                                                                                                                                                                    217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503
                                                                                                                                                                                                                                                                                                                                                703
                                                                                                                                                                                                                                                                                                                                                                                                          653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
```

```
alignment_block:
US-10-040-803-7 x AF321182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1720.00
Ratio: 5.426
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AF321182 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AF321182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pr:AF321182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBMED
          168
                                                                               118 GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
34 rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal
                                                                                                                                                             68 CTTCACCTCCTGCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCA
                                                                                                                                                                                  17 rPheThrSerLeuLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA
                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                  1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyGlyCysLeuGlyTh
                                                                                                                                                                                                                                               ATGGTGGTTTCTGGAGCGCCCCCAGCCCTGGGTGGGGGGCTGTCTCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-NOV-2000) Rheumatology, Immunology and Allergy, Brigham and Women's Hospital, Harvard Medical School, 1 Jimmy Fund Way, Boston, MA 02115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wong, G.W., Yasuda, S., Madhusudhan, M.S., Li, L., Yang, Y., Krilis, S.A., Sali, A. and Stevens, R.L. Human Tryptase epsilon (PRSS21), a New Member of the Chromosome 16pl3 3 Family of Human Serine Proteases Expressed in Airway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong, G.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 276 (52), 49169-49182 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 1332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF321182.1 GI:11386012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF321182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 1332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="myvsgappalgggclgtftsllllastailnaaripyppacgkp
QQLNRVvggeb5DsEwpwivsiQKngthHCAG5L125WWithAHCEKDNLNKPYLF
SVLLGAWQLGNPGSRSQKVGVAWPEHPVYSWKEGACADIALVRLERSIQFSERVLPI
CLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQ
GPITEDMLCAGYLEGEBDACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQGSGAAARS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="serine protease PRSS22"
/protein_id="AAG35070.1"
/db_xref="GI:11386013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pancreas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1332 bp mRNA
cease PRSS22 mRNA,
                                                                                                                                                                                                                                                                                                                             to: 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                       50
  217
                                                                                  167
                                                                                                                                                               117
                                                                                                                                                                                                     34
                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI 26-DEC-2001
```

```
seq_name: gb_pr:BC009726
            ACCESSION
                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                             818
                                                                                                                                                                                                                                                                                                                                                                                       718
                                                                                                                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                                                                                                                                           899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                    301 GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaAlaArgSe 317
                                                                                                                                                                                                                           838
                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167
                                                                                                                                                                                                                                                    284
                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                           GGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCCTCAGGGG
                                                                                                                                                                                                                                                                             luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACCTCCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTGATGCCTCAT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTTCTCTGTGCTGGGGGGGCCTGGCAGCTGGGAACCCTGGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT
                                                                                                                  G
                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTTGGAGGGGG
                                                                                                                                                                                                                                       rpValGluLysI1eValGlnGlyValGlnLeuArgGlyArgAlaGlnGly
                                                                                                                                             r 317
                                                                                                                                                                      896
         Homo sapiens, protease, mRNA, complete cds. BC009726
BC009726.1 GI:16307274
                                                     BC009726
                                       serine,
                                                     1403
                                                   đđ
                                     mRNA linear
22, clone MGC:9599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
                                                                                                                                                                                                                                                                                 867
                                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                                                                                                         767
                                                                                                                                                                                                                                                                                                                                                                                                                                              717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217
                                                                                                                                                                                                                            917
                                        PRI 22-OCT-2001
IMAGE:3899480,
```

```
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                      Align seg 1/1 to: BC009726
                                                                                                                                                                                                                                                          US-10-040-803-7 x BC009726
                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
39
                                                                                                                                 1 MetvalvalSerGlyAlaProProAlaLeuGlyGlyGlyGlyCysLeuGlyTh 17
                                                                                                   ATGGTGGTTTCTGGAGCGCCCCAGCCCTGGGTGGGGGGCTGTCTCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: 1 Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 11545838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthería; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          Quality: 1720.00
Ratio: 5.426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQLINRVVGGEDSTDSEMPWIVSIQKNGTHHCAGSILITSRWVITAAHCFKDNLNKPYLF
QQLINRVVGGEDSTDSEMPWIVSIQKNGTHHCAGSILITSRWVITAAHCFKDNLNKPYLF
SVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPI
CLPDASTHLPPWHCWISGWGSLQDGVVEPHPQVTLQHPIIDSEVCSHLYWRGAGQ
GPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYI
SLSAHRSWYEKIVQGVQLRGRAQGGGALRAPSQGSGAAARS"

452 c 410 g 266 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="protease, serine, 22"
/protein_id="AAH09726.1"
/db_xref="GI:16307275"
/translation="MYVSGAPPALGGGCLGTETSLLLLASTAILNAARIPVPPACGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="LocusID:64063"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Pancreas, epithelioid
/clone_lib="NIH_MGC_70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="MGC:9599 IMAGE:3899480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1403
                                                                                                                                                                                                            from: 1 to: 1403
                                                                                                                                                                                                                                                                                                                                     Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pcmv-sport6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinoma"
                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found
```

```
689
                                                                                                                                           688
                                                                                                                                                                                                                  839
                                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       639
989 C 989
                                                                                                       301
                                                                                                                                                                                                                                                                                      789
                                                                                                                                                                                                                                                                                                                        251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                                                                                                                                                           /39
                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                 r 317
                                                                 rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly
                                                                                                                                                                                                                               aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT
                                                                                                                                                                                                                                                                                                                                                        AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                         GGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGGGG
                                                                                                                                                                                                              CGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCGCACCGCTCCT
                                                                                                                                                                                                                                                                                    GACGGCGCCTGGCTGGCCGGCATCATCAGCTGGGGGCGAGGGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaG1 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACCTCCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ### ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTTCTCTGTGCTGCGGGGGGCCTGGCGAGCTGGGGAACCCTGGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGATGGAGTTCCCTTGCCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCCAGAAGGTGGGTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTGATCACTGCCGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT 188
                                                                                                                                                                           300
                                                                                                                                                                                                              888
                                                                                                                                           938
                                                                                                                                                                                                                                                                                    838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
```

seq_name: gb_ro:AB010778

```
JOURNAL REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block: LOCUS AB010778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                              US-10-040-803-7 x AB010778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
230 GTGGGAGGTGAGGACAGCATGGATGCCCAGTGGCCCTGGATTGTTAGCAT
                                                                                                                                                                                  130 CTTAATCCTTCTGGTGCTGCTGACTTCCACAGCTCCCATCAGTGCTGCCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                        51 ValGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67
                                                                                                                34 rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal
                                                                                                                                                                                                                                                                      1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh
                                                                                        CCATCCGAGTGTCCCCCAGACTGTGGGAAGCCTCAGCAGCTGAACCGGATT
                                                                                                                                                                                                                           rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1275.5
Ratio: 4.621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-Jan-1998) Nozomi Yamaguchi, Institute for Geriatrics, Kyoto Prefectural University of Medicine, Department of Cell Biology; Kajii-cho 465, Kamigyo-ku, Kawaramati Hirokoji, Kyoto, Kyoto 602-6566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp, Tel:81-75-251-5848(ex.5848), Fax:81-75-251-5848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitsui,S., Okui,A., Kominami,K. and Yamaguchi,N. Cloning and characterization of a novel serine puppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1321)
Yamaguchi, N. and Mitsui, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus brain cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB010778.1 GI:12248748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete cds.
AB010778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus mBSSP-4 mRNA
                                                                                                                                                                                                                                                                                                                                                                 ç.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280
                                                                                                                                                                                                                                                                                                                                                                 AB010778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="brain specific serine protease-4"
/product="brain specific serine protease-4"
/product="Ba820262.1"
/db_xref="Gi:12484749"
/db_xref="Gi:12484749"
/translation="MMISRPPPALGGDQFSILILLVLLTSTAPISAATIRVSPDCGKP
QQLNRIVGGEDSMDAQWFWIVSILKNGSHHCAGSLLTRWWVTRAHCFKSNMDKPSLF
SVLLGANKLGSPGPRSQKVGIAWVLHPHPXTSWEGSTHADIALVRLEHSIGVSERILPI
CLPDSSVRLPRKTDCWIAGWGSIQDGVPLPHPQTLQKLKVPIIDSELCKSLYWRGAGQ
CAITEGMLCAGYLEGERDACLGDSGGPLMCQVDDHWLLTGIISWGEGCADDRPGVYTS
LLAHRSWVGRTVQGVQLRGYLANSGDTGSS"
LLAHRSWVGRTVQGVQLRGYLANSGDTGSS"
375 c 372 g 294 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="mBSSP-4"
80. .1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="prosemin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="mBSSP-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 50
                                                                                                                                                                                                                                                                                                                                                                 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 2
Percent Identity: 75.641
                                                                                                                                                                                                                                                                                                                                                                 ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1321 bp
NA for br
                                                                                                                                                                                                                                                                                                                                                                 ţo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protease, mBSSP-4
                                                                                                                                     50
                                                                                                                                                                                                                             34
279
                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease-4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROD 17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae; Mus.
```

```
seq_name: gb_ro:RRA5642
                                                       SOURCE
                                                                       KEYWORDS
                                                                                             VERSION
                                                                                                                                 DEFINITION
                                                                                                               ACCESSION
                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                           284 rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly 300
                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730 TCAGGAAGCCATCACGGAGGGCATGCTGTGTGCTGGTTACCTGGAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                 301 Gly.GlyAlaLeuArgAlaProSerGlnGlySer 311
                                                                                                                                                                                                                                                                                                                                                                                               880 GGAC...GACCGGCCCGGTGTGCACCACCACCCTCCTAGCTCACCGCTCCT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167
{||||||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATCATCGACTCCGAACTCTGCAAAAGCTTGTACTGGCGGGGAGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGTCTCCCTAGACCGACTGCTGGATTGCCGGCTGGGGAAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCAGTTCTCTGAGCGGATCCTGCCCATCTGCCTACCTGACTCCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAAGGAGGGAACCCATGCAGACATTGCCCTGGTGCGCCTGGAACACTCC 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCCAGAAAGTAGGCATTGCTTGGGTGCTGCCTCACCCCAGGTATTCTT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTTCTCAGTATTGTTGGGGGGCCCTGGAAGCTGGGGAGCCCAAGGCCCAAG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                               AGTGGGGACACAGGAAGCTCCTAATCTAGGATCT 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGATGGAGTGCCCCTGCCCCACCCTCAGACCCTTCAGAAGCTGAAGGTG
                                                                                                                                                                                                                                                                                                                       GGGTGCAAAGGATCGTTCAAGGGGTGCAGCTGCGGGGTACTTGGCGGAC 976
                                                                                                             Rattus rattus mRNA encoding brain serine protease bsp2, AJ005642
                                                     bsp2 gene; serine protease.
black rat.
                                                                                           AJ005642.1 GI:3559979
                                     Rattus rattus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  779
                                                                                                                                                     ROD 07-SEP-1998
```

```
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-10-040-803-7 x RRA5642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: RRA5642 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                         175 TCGCCAGATTGTGGGAAGCCGCAGCAGCTGAACAGGGTCGTGGGAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 TCTTTATTCTCTTGCCCTCAGCCACAGTCAGTGCAGCCAACATCCGAGGG 174
                                                                                                                                                                      54 uAspSerThrAspSerGluTrpProTrpIleValSerIleGlnLysAsnG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 euLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIleProVal
                                        71 lyThrHisHisCysAlaGlySerLeuLeuThrSerArgTrpVallleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 GGGGATCCCCAGGCATGGGGCACGGGGTTCATCACCACCAGGACTAACCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyThrPheThr.SerL 21
                                                                                                                                                                                                                                                                                                                                                      ProproAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyGlyGl 54
                                                                                                                              GGACAGCGCGGATGCCCAGTGGCCTTGGATCGTTAGTATCCTCAAGAACG
Direct Submission
Submitted (17-ApR-1998) Lathe R., Ctr. for Genome Research and for Neuroscience, University of Edinburgh, West Mains Road, Edinburgh, EH9 3JQ, UNITED KINGDOM
2 (bases 1 to 1259)
Davies, B.J., Pickard, B.S., Steel, M., Morris, R.G. and Lathe, R. Serine proteases in rodent hippocampus
Serine proteases in rodent hippocampus
Serine Chem. 273 (36), 23004-23011 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1223.00
Ratio: 4.668
milarity: 87.625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98389725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lathe, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="bsp2"
163. 984
/gene="bsp2"
/product="serine protease"
a 352 c 362 g 282 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
/tissue_type="hippocampus"
/dev_stage="adult"
<94..162</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPGPRSQKVGIASVLPHPRYSRKEGTHADIALVRLERPIQFSERILPICLPDSSVHLP
PNTNCWIAGWGSIQDGVPLPRPQTLQKLKVPIIDPELCKSLYWRGAGQBAITEDMLCA
GYLEGKRDACLGDSGGPLMCQVDDHWLLTGIISWGEGCAERNRPGVYTSLLAHRPWVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="<94...9</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="serine protease"
/product="serine protease"
/protein_id="CAA06644.1"
/db_xref="GI:355980"
/db_xref="GI:355980"
/db_xref="GI:355980"
/db_xref="GI:355980"
/db_xref="GI:355980"
/db_xref="GI:355980"
/db_xref="GI:355980"
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQQLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQQLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQQLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQLLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQQLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQLLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQLLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQLLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQQLNRVVGGE
/translation="ARGSSPPGLTLFILLPSATVSAANIRGSPDCGKPQQLNRVVGGE"
/translation="ARGSSPPGLT"
/translation="A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="BSP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Fisher"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus rattus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIVQGVQLRGRLADSGDTGSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="bsp2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bsp2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 75.585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                           274
                                                                                                                                                                                                                                                                                                                       224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ctr.
```

```
REFERENCE
AUTHORS
                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                seq_name: gb_pr:AC003965
                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                        ERSION
                                                                                                                                                                                                                                         ACCESSION
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                    288 IleValGlnGlyValGlnLeuArgGlyArgAlaGlnGlyGlyGly 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 rgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpValGluLys 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 alGlyValAlaTrpValGluProHisProValTyrSerTrpLysGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 lLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLysV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGluArgAsnA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAspGlyAlaTr 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyGluArgAspAla 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProLeuProHisProGlnThrLeuGlnLysLeuLysValProIleIleAs 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGluArgValLeuProIleCysLeuProAspAlaSerIleHisLeuProP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaCysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSe 154
                                                                                                                                                                                                                                                                                                                                                                  ATCGTGCAAGGGGTGCAGCTGCGAGGGGCGCTTGGCGGACAGTGGG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCCGGCGTGTACACCAGCCTCCTAGCTCACCGCCCCTGGGTGCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCACCGAGGACATGCTGTGTGCTGGTTACCTGGAAGGGAAGCGGGACGCT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSerGluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGlyProI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACACCAACTGCTGGATTGCCGGCTGGGGAAGCATCCAGGATGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCCATGCAGACATTGCCCTGGTGCGCCTGGAACGCCCCATCCAATTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTCTGGGCGACTCTGGGGGGTCCCCTGATGTGCCAGGTGGATGACCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTGAACTCTGCAAAAGTTTGTACTGGCGGGGAGCTGGTCAGGAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roAsnThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyVal 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGGCATTGCTTCGGTGCTGCCCCACCCCAGGTATTCTCGGAAGGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGTTGGGGGCCTGGAAGCTAGGGAACCCAGGCCCAAGGTCTCAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGCACACTGCTTTAGCAGCAATATGGACAAACCATCTCCGTACTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAlaHisCysPheLysAspAsnLeuAsnLysProTyrLeuPheSerVa 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCCCACCACTGCGCAGGCTCCTTGCTCACCAACCGCTGGGTGGTCTCA 324
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34642)

Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J. and Deaven,L., Sequencing of Human Chromosome 16p13.3
                                                                                                                                                                                                                                                      Homo sapiens chromosome
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                         AC003965
                                                                                                                                                                                 human.
                                                                                                                                                                                                                      AC003965.1
                                                                                                                                                                                                                    GI:2734091
                                                                                                                                                                                                                                                                    34642 bp
                                                                                                                                                                                                                                                      16,
                                                                                                                                                                                                                                                     2 bp DNA cosmid clone
                                                                                                                                                                                                                                                 linear PRI 31-DEC-199 325D7, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374
                                                                                                                                                                                                                                                                    PRI 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                            CDS
                                                                                                gene
                                                                                                                                   misc_feature
                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence submitted by:
DOE Joint Genome Insti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 34642)
Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
Ricke,D.O., Dones,M., Buckingham,J., Chasteen,L., Thompson,S.,
Robinson,D., Jones,M., Buckingham,J., Meincke,L., Longmire,J.,
Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J.,
White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J. and Deaven,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 34642)
Ricke, D.O., Wagner, R.P. and Mundt, M.O.
Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Institute, Los Alamos National Laboratory, MS M888, Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (31-DEC-1997) Center for Human Genome Studies, DOE Joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Joint Genome Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_fami.
9672. .97
                                                                                                                                                                  complement(14456.
                                                                                                                                                                                                            /rpt_1
13964.
                                    /evidence=not_experimental
join(<17398. .17540,17771. .18048,19600.
                                                                                          /rpt_family="Alu"
16240. 16446
/note="458 Swiss-Prot:P18127"
join(<17398. 17540,17771. .18048,19600.
                                                                                                                                                                                                                           complement(11793.
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                           complement(10884.
 /note="putative serine protease"
                       /gene="SP001LA"
                                                                             join(<17398. .1'
/gene="SP001LA"
                                                                                                                                                                                         /rpt_family="MIR"
                                                                                                                                                                                                                                                                /rpt_family="Alu"
                                                                                                                                                                                                                                                                                     /rpt_family="Alu"
11493. .11799
                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
11211. .11522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
complement/co...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(8846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (6664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alu" 3105. .3373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1803
                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
5206, K510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
2626. .2809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_fam:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="16p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .34642
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="MSTc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="325D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="MLT1b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="Alu"
ement/100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="Alu"
                                                                                                                                                                                                            14098
                                                                                                                                                                                                                                                                                                                                                                                                   10674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ly="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                   ly="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y="MSTc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2246)
                                                                                                                                                                     .14468)
                                                                                                                                                                                                                                                 .12160)
                                                                                                                                                                                                                                                                                                                                                             .11179)
                                        .19757,20293.
                                                                                            .19757,20293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500
```

.20878)

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                    Align seg 1/1 to: AC003965 from: 1 to: 34642
                                                                                                                                                                                                                                                                                                       US-10-040-803-7 x AC003965
                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                       hent_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epeat_region
                                                                                                                                                                                                                                                                                                                                                       Quality: 1094.50
Ratio: 3.895
milarity: 26.635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="SP001LA"
/product="SP001LA"
/protein_id="AAB93671.1"
/protein_id="AAB93671.1"
/db_xref="Gi:2734092"
/db_xref="Gi:2734092"
/translation="LNRVVGGEDSTDSEWPWIVSIQKNGTHHCAGSLLTSRWVITAAH.
/FIRNSVLIGAWQLGNPGSRSQKVGVAWVEPHPVTSWKEGACADIALVRLE
RSIQFSERVLPICLPDASILLPNTHCWISGWGSIQDGFDLPHPQTLQKKVPIIDSE
VCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLLAGIISWGE
GCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQGSGAAARS"
complement(18257...18556)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="MER4"
27294. 27592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Serine Protease SP002LA catalytic exon B"
33314...33474
/note="Serine Protease SP002LA catalytic exon C"
33691...33966
/note="Serine Protease SP002LA catalytic exon D"
1 9148 c 8812 g 8895 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alu"
complement(25703.
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(24599. .25217)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Serine Protease SP002LA catalytic exon A" 32602. .32780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(30340. .30649)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(29107. .29227)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Alu" complement(27650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(26818. .26888)
/rpt_family="LTR8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (25525. .25603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(22376.
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(22028. .22333)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-"SP001LA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MER4b"
complement/orial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .32459
                                                                                                                                                                                                                                                                                                                                                       Gaps: 5
Percent Identity: 26.635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8812 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .22722)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .26005)
                                                                                                                                                                                                                                                                                                                                                                                         Length:
```

186		2
18464	CCTGGCTAATTTTTGTATTTTTTGTAGAGACAGGGTTTTTCTGTGTTTGGC	18415
186		186
18414	TCCCACCTCAGCCTCCCAGGTAGCTGGAACTACAGGTGTGTGCTACCACA	18365
186		186
18364	GGTGTGATCCTAACTCACTGCAGCCTTTGCCTCCCAGGCTCAAGTGATCC	18315
186		186
18314	TTTTTTTTTGAGACAGGGTGTTACTCTGTCACCCAGGCTGGAGTGCAGT	18265
186		186
18264	ATTTCAGGCCATTTCTCTTTTCTTTCTTTCTTCTTCTTCTTTTTTTT	18215
186		186
18214	AGAGGTGGAAGGAAAGATGGGCTGCAATCCAGAAGAAACCTTGGTGGGCA	18165
186		186
18164	ACACAGACACCATGAGCAACAAAGGGTGGAGGCCAGAGGCACAGCATGAC	18115
186		186
18114	TCCAAGGTGGTTGGGGGCAGATGGGGACAGAGGATGGCAGACACTCAGGG	18065
186		186
186 18064	TrpIleSerGlyTrpGlySerIleGlnAspGly	176 18015
00	CATCTGCCTACCTGATGCCTCTATCCACCTCCCTCCAAACACCCCACTG	17965
75	roIleCysLeuProAspAlaSerIleHisLeuProProAsnThrHisCys	159
159 17964	eAlaLeuValArgLeuGluArgSerIleGlnPheSerGluArgValLeuP 	142 17915
142 17914	ValGluProHisProValTyrSerTrpLysGluGlyAlaCysAlaAspIl 	126 17865
7	GCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAGGTGGGTG	17815
125	rglnLenglvAsnProglvSerArgSerGlnLvsValGlvValAlaTr	
17814	.aspasnieuasniysPoOTyrieuPheSerValieuLeuGlyAlaT .aspasnieuasniysPoOTyrieuPheSerValieuLeuGlyAlaT .TrocagcaaccrgaacaaccaraccrgoTTCTCGTGCTGCTGGGGGGCCT	94 17765
7	CTTTC	17715
93		93
17714	CCTAGAAGCCTCTCCTGCCTTCAGGGGCCTTCACACCCATGCTGTTCCCC	17665
93		93
17664	ACAGGCTCTGCTTCCGGGCCTCTGTTCAATCTTGGTGCCCCTCGATTCTA	17615
93		93
17614	TIGATCTICTAAGGCCCTGGGCTTTGTGCCCCAGGCCCCTGGGCTCCCTTT	17565
93		93

OOT

186		186
19364	ATGCAGTATCTGAGACAGGAAGGGCTCTAACCATCTGTGGATATAAGAAA	19315
186		186
19314	GACATTTATTGAACACTTCTTCTATAGCAGTCCCAGTGCTGGATGAAGTA	19265
186		186
19264	AGGCAAGGCGTGGGGATCCCTCAGGTCCTGGTAATTTTCAACATCGAGTG	19215
186		186
19214	CGCGGACTTTCAGTCCACAATCTGCAGACCACAGTCTGTAGACCAGCTCC	19165
186		186
19164	GGTTGCAACCTCTCCATGATCTCTGTAGGGGCTTCTTCAAGAGCTAGAAT	19115
186		186
19114	TTAAGAGAAATGACACTAGCTCAGGTGTGTGGGGGATCCCCAGTAACTCTGA	65
186		186
19064	GTAATAACAAAGTGTAAGACAGATGAAAATTTAACCAGATTCCAGAATAA	19015
186		186
19014	TACAATGAAGACCTGGAAGAAAGAGTTTGAAAGAGAGAGCTAGAGACTAA	18965
186		186
18964	GATGATAGAGACTGGGCCAAGGAAAAGAAACATACAGGCAGAAATGAGGA	18915
186		186
18914	AAGCAGGGAAGCAAGAGAAAGGTAGATGACAGATCGACAGGCAGATG	18865
186		186
18864	AGGTTTGGAAAACATCATCTCAAAACTCAAACTAGATTACATAAAGCAAG	18815
186		186
18814	GAAAATGCAGCCACCTTAATTGTAAAATATAATTTTCAAACCACCACTGG	18765
186		186
18764	AGGCACCCCTGGTGGTAGCATGCCACAATTGCGGGCAAAATTCTCGGGA	15
186		186
18714	TAAGCTGAATACAGGGTGAATATAAAGAGGCCTGATTCCAGAGTGGGAAC	18665
186		186
18664	CTATTCAATTCATCAATACAGGAATGGCTGAAAGGGGGTGTGTGT	18615
186		186
18614	ACTTCAAAAGTATCTGGCTATGTTTTGAGGCAACAGCCAGACCCGTGAAG	18565
186		186
18564	CCAAAGTGCCGGGATTACAGGTGTGAGCCACTGTGCCTGGCCTCATTTCT	18515
186		186
18514	TGGGCTGGTCTTGAACTGTTGGGCTCAAGCAATCCACCAGCCTCAGCCTC	18465

20314	SACTCCGGGGGCCCCCTCA	20265
247		240
20264	CCCCCTGACAGGGCACGGGCCCTGGATTCTGCCACCCCCTGTGCCACGGG ;	20215
239		239
20214	CCTGTCTCCTCCAGGAAGGAGAAACGGGCTCCCGGGAAGGGGGCTCATCTG	20165
239		239
20164	GCAGCTCCTACTCTGCCGCCGGGGACTTCTCACCTGGGTGGAGCTCAGGT :	20115
239		239
20114	TCAGATGGTGCAGCGGCAGCACCCGCGCCTGGACGTCTTAAGGCCTGGCT	20065
239		239
20064	CGCCTCAGTGCCCAGAGCCAGCTGTAGCTCAGGGGCTGTCTGGAAGACGG	20015
239		239
20014	TGCACCACCTCGCCTCCGCGAGCTTTCATTTCCTTCAGGGGGCCTTCCCCA	19965
239		239
19964	TGGCTCAGCCACTTATTTGTTCAGACATTAAACTGGGCATCCCAGC	19915
239		239
19914	GAACTGGCTGTGCCTGACAGTCCCGGGTCCCCATAGAACCAGCCTCAGCC	19865
239		239
19864	TCAGTCCTGTCCCCACTGAGCCCCACAACCTCTCCCCTGGCCTCCCTC	19815
239		239
19814	CCCTCGAGCCCCCACCCCTGGCCAGGAGGGCCTCGGGAAGGAGCCAGCG	19765
239		239
239 19764	tLeuCysAlaGlyTyrLeuGluGlyGluArgAspAlaCysLeu	225 19715
225 19714	SerHisLeuTyrTrpArgGlyAlaGlyGlnGlyProIleThrGluAspMe 	209 19665
208 19664	roGlnThrLeuGlnLysLeuLysValProIleIleAspSerGluValCys 	192 19615
19614	ACCCCCAAACCTGATTCTGTCCTCTTTCCTCCCAGTTCCCTTGCCCCACC	19565
192	His	187
19564	GAATGGTGTTGGGGGGGAATAGTCCTTTGAGGAGGCAACGAGGAGGG	19515
186		186
19514	GAGAGACTGGTAGAGCTAATCTGTTAGCCTTTGAGAACCGCTGCTGAGAG	19465
186		186
19464	CAGGGCCAGAGGTGGAGACCTGGAATTTTCAATTTTCTGAAGGCATCTTG	19415
186		186
19414	ATTTATTAAAGAGGTAGGGTCTTAGGTTTCACATTCATGTTCTAATTCAG	19365

```
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20365 GAGGGCTGTGCCGAGCGCCAACAGGCCCGGGGTCTACATCAGCCTCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lame: gb_pr:HSA306593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AlaAlaArgSer 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     §15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rgAlaGlnGlyGlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAla 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aHisArgSerTrpValGluLysIleValGlnGlyValGlnLeuArgGlyA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluGlyCysAlaGluArgAsnArgProGlyValTyrIleSerLeuSerAl 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGCTCAGGGGGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGCGCGCTCC 20526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ306593.1 GI:13516325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1013) Fortunato, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fortunato, M., Dando, P.M., Rawlings, N.D. and Barrett, A.J. Cloning, sequencing and expression of marapsin, a human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  marapsin; MPN gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens mRNA for marapsin (MPN gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-MAR-2001) Fortunato M., MRC Molecular Enzymology Laboratory, Babraham Institute, Babraham Hall, Babraham, Cambr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory, Babraham Institute, Babraham CB2 4AT, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Related entry AW170323
                                     Ratio:
                                                                                                                                                                                                                                                    192
                                                                                                                                                                                                                                     /product="marapsin"
/protein_id="CAC35467.1"
/protein_id="CAC35467.1"
/db_xref="CAC35467.1"
/db_xref="CAC35467.1"
/db_xref="CAC35467.1"
/db_xref="CAC35467.1"
/db_xref="CAC35467.1"
/db_xref="CAC35467.1"
/db_xref="CAC35467.1"
/ref="CAC35467.1"
/ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE 2698030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
739.00
3.421
75.789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="MPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="putative trypsin-like activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 892
       Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1013 bp
                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
   48.772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 31-MAR-2001
```

```
alignment_block:
US-10-040-803-7 x HSA306593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: HSA306593 from: 1 to: 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 AGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCATCCAGCGCAAC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 alLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLys 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 GGCTGCGCACTGCTTCCGC...AACACCTCTGAGACGTCCCTGTACCAGG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 ProAsnThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyVa 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 erGluArgValLeuProIleCysLeuProAspAlaSerIleHisLeuPro 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 GCCCGGGTGAGGCAGGTGGAGAGCAACCCCCTGTACCAG...GGCACGGC
283 rTrpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnG 300
                                                                                 267 AlaGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSe 283
                                                                                                                                                      729
                                                                                                                                                                                                                                                                        629 CAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              579 ACACACCCAAGTGCAACCTGCTCTACAGCAAAGACACCGAGTTTGGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529 CCTCCTGCCCGAACCGCGGATCCTGCAGAAACTCGCTGTGCCCATCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 rAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyrLeuPheSerV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 GlyThrHisHisCysAlaGlySerLeuLeuThrSerArgTrpValIleTh 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 luAspSerThrAspSerGluTrpProTrpIleValSerIleGlnLysAsn 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 lProProAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyGlyG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 CTGCTGCTGTGT.....TTTGGGTCTCAGAGGGCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIleProVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCCTTCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yAlaCysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGlyValAlaTrpValGluProHisProValTyrSerTrpLysGluGl 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGCTGGGGGCAAGGCAGCTAGTGCAGCCGGGACCACACGCTATGTAT 331
                                                                                                                                                                                                                                                                                                                                                                                             .....ProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGGGCATGAACTGCTGGGTCACTGGCTGGGCCAGCCCCAGTGAGGAAGA 528
                                                  GCCCGCCAGAACCGCCCAGGTGTCTACATCCGTGTCACCGCCCACCACAA
                                                                                                                                                 TGGGTCAGTCGTGGCTGCAGGCGGGGGGGTGATCAGCTGGGGTGAGGGCTGT 778
                                                                                                                                                                          alAspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCys 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spSerGluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGly...
                                                                                                                                                                                                                                                    CAAGAAGGATGCCTGCAAGGGCGACTCGGGCGCCCCCTGGTGTGCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                                                                                                                     233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378
                                                                                                                                                                                                                                                                                                       250
                                                                                                                                                                                                                                                                                                                                                       678
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                            Align seg 1/1 to: AB018694
                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_ov:AB018694
                                                                                                                                                                                                                          US-10-040-803-7 x AB018694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
123 TGGACAGTAAGAGGGGGGAATGGCCTTGGCAGATAAGCCTGAGCTACAAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RENCE
                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORS
                                       54 luAspSerThrAspSerGluTrpProTrpIleValSerIleGlnLysAsn 70
                                                                                                              38 ProPro.AlaCysGlyLysProGlnGlnLeuAsnArgValValGlyGlyG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 lyGly 301
                                                                                       CCACCAAGCCTGTGGTGTACCAGTAATATCAAATCGCATTGTTGGGGGGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGC 883
                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (15-OCT-1998) Kazuto Yamada, Graduate School of Human Informatics, Nagoya University; Furo-cho, Chikusa-ku, Nagoya 464-8601, Japan (E-mail:yamadait@info.human.nagoya-u.ac.jp, Tel:+81-52-789-2572, Fax:+81-52-789-2567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The expression control of xepsin by non-axial and planar posteriorizing signals in xenopus epidermis Unpublished (1998)
2. (bases 1 to 2078)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis neurula cDNA to Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada, K., Takeshima, K. and Takabatake, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermis specific serine protease; xepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB018694.1 GI:6009514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis Xepsin mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ramada, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB018694
                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                              603 a
                                                                                                                                                                                                                                                                                      661.50
3.227
72.695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="epidermis specific serine protease"
/protein_id="BA884941.1"
/protein_id="BA884941.1"
/db_xref="GI-609515"
/translation="MLOYLSFVLIFIHHQACGVPVISNRIVGGMDSKRGEWPWQISLS
YKSDSICGGSLLTDSWVMTAAHCIDSLDVSYYTVYLGAYQLSAPDNSTYSRGYKSITK
HDDFOYEGSSGDIALIELEKPVTFTPYILPICLPSQDVQFAAGTMCWVTGWGNIQEGT
PLISPKTIQKAEVAIIDSSVCGTMYESSLGYIPDFSFIQEDMYCAGYKEGRIDACGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVAPSIGPSIAPSFGPSLGPRGVASTTISQTEAQSVNSIEIDKTNSTTIFETEAMSMS
NNTTMMETFSLVSSTISTALRINETKTIDNEAQIHACSLHTIALTLIYLFIRFFV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGPLVCNVNVWLQLGIVSWGYGCAEPNRPGVYTKVQYYQDWLKTNVPLIVFSEEGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="neurula" 35. .1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Xepsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                              455 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xepsin"
                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                      Percent Identity: 47.163
                                                                                                                                                                                                                                                                                                                                                                                                                                              437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2078
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                            ţo:
                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  đđ
                                                                                                                                                                              2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermis specific serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRT 05-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease,
```

```
seq_documentation_block: LOCUS AX098193
                                     KEYWORDS
                                                           VERSION
                                                                                 ACCESSION
                                                                                                     DEFINITION
                                                                                                                                                                               seq_name: gb_pat:AX098193
  ORGANISM
                                                                                                                                                                                                                             855 AAGGACCAAGTGTT...GCACCAAGCATTGGACCAAGCATTGCA
                                                                                                                                                                                                                                                                   300 lyGlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAla 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  614 GATTTCAGCTTCATTCAGGAGGACATGGTGTGTGCTGGTTACAAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                283 rTrpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 ACAGTTCAGTCTGTGGGACCATGTACGAATCCAGCTTGGGCTACATCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 spSerGluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 CCCTTTAATCAGCCCTAAAACTATTCAGAAGGCAGAAGTTGCCATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 lProLeuProHisProGlnThrLeuGlnLysLeuLysValProIleIleA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 GCAGGGACTATGTGCTGGGTGACTGGGTGAGGAATATTCAAGAAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 CCCCTTACATCCTACCCATCTGCCTTCCCTCTCAGGATGTTCAATTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 erGluArgValLeuProIleCysLeuProAspAlaSerIleHisLeuPro 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ValGlyValAlaTrpValGluProHisProValTyrSerTrpLysGluGl 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 alLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLys 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 TGCTGCTCACTGCATT...GATTCGTTGGATGTTTCATAC...TATACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alAspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGTTGAAA....ACCAATGTGCCTTTAATTGTGTTCAGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                              GCAGAACCCAATAGACCTGGTGTCTATACCAAAGTTCAGTATTACCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAACAATGTCTGGCTTCAGCTCGGTATTGTGAGCTGGGGATATGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProAsnThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyVa 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....IleThrGluAspMetLeuCysAlaGlyTyrLeuGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCAGTGGTGACATTGCTCTAATTGAACTGGAGAAACCTGTCACTTTTA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yAlaCysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGGAGTGAAAAGTATAACAAAGCACCCAGATTTCCAATAC...GAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATCTCGGTGCATATCAGCTCTCTGCCCCTGACAATTCTACAGTATCC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyrLeuPheSerV
Homo sapiens
                                                                               Sequence 105 from Patent W00118542
AX098193
                   human
                                                           AX098193.1 GI:13515276
                                                                                                                      ģ
                                                                                                                      DNA
                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                              813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463
                                                                                                                                                                                                                                                                                                            854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                                                                                                                                                                                                                                                                     283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266
                                                                                                                      PAT 30-MAR-2001
```

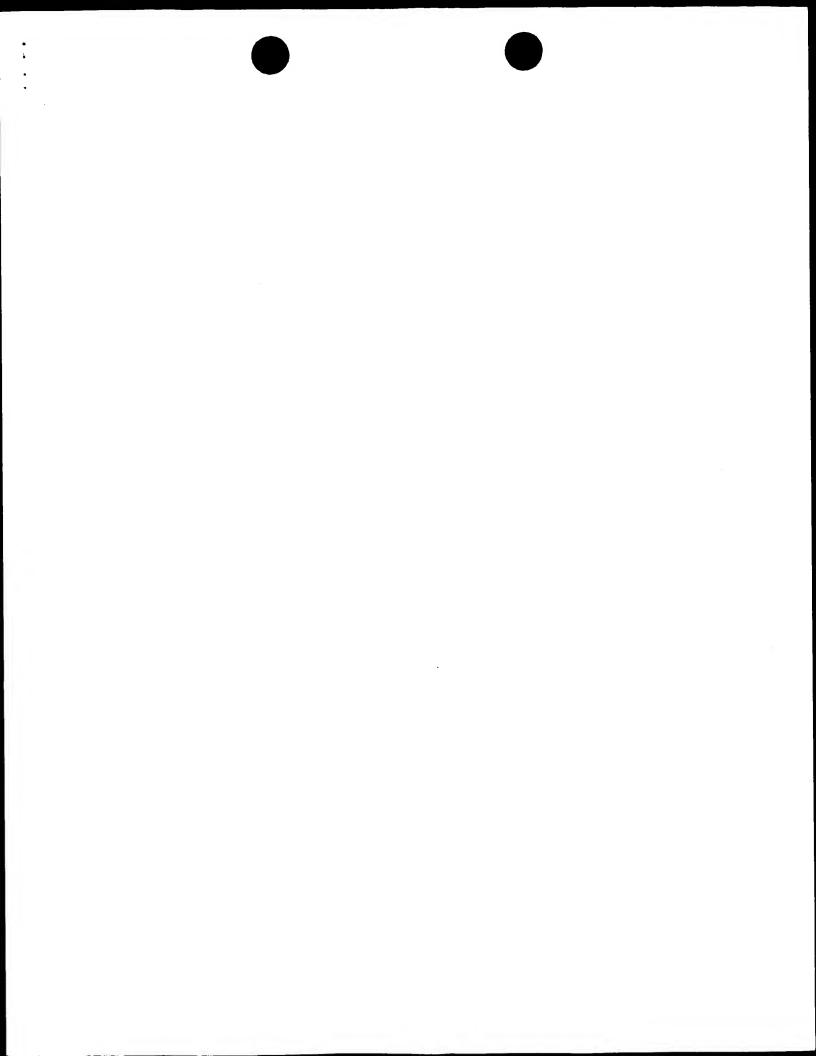
SOURCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AX098193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                          190
                                                                                                                                                                                                               173 rHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyValProLeuP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                 140 laAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSerGluArg 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 GAAGGACATCATCCCCCACCCCAGCTAC...CTCCAGGAGGGCTCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 lAlaTrpValGluProHisProValTyrSerTrpLysGluGlyAlaCysA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
  207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ent_block:
-040-803-7 x AX098193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 ACTGCTTCCCCAGCGAGCACCACAAGGAA...GCCTATGAGGTCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 uLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIleProValProProA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LeuGlyGlyCysLeuGlyThrPheThrSerLeuLeu.....Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrAspSerGluTrpProTrpIleValSerIleGlnLysAsnGlyThrHi 73
ValCysSerHisLeuTyrTrpArgGlyAla...GlyGlnGlyPro....
                                                                                                                                                          CACTGCACTGTCACTGGCTGGGGTCATGTGGCCCCCTCAGTGAGCCTCC
                                                                                                                                                                                                                                                                       ATCCGGCCCATCTGCCTCCCTGCAGCCAACGCCTCCTTCCCCAACGGCCT
                                                                                                                                                                                                                                                                                                                       ValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAsnTh 173
                                                                                                                                                                                                                                                                                                                                                                                 GCGACATTGCACTCCTCCAACTCAGCAGACCCATCACCTTCTCCCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGCCCACCAGCTAGACTCCTACTCCGAGGACGCCAAGGTCAGCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLysValGlyVa 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGTGTGGGGCTCTCTCGTGTCTGAGCAGTGGGTGCTGTCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sHisCysAlaGlySerLeuLeuThrSerArgTrpValIleThrAlaAlaH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCGCCGGTCAGTGGCCCTGGCAGGTCAGCATCACCTATGAAGGCGTCCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laCysGlyLysProGlnGlnLeuAsnArgValValGlyGlyGluAspSer 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCCGGTCGGGACAGGAGCGGAAGGGGCAGAAGCTCCC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGGGCCTGGGCAGCTGGGGCCTGTGGCCATTCTGCTCTATCTTGGATT
                                                        TGACGCCCAAGCCACTGCAGCAACTCGAGGTGCCTCTGATCAGTCGTGAG
                                                                                                       {\tt roHisProGlnThrLeuGlnLysLeuLysValProIleIleAspSerGlu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isCysPheLysAspAsnLeuAsnLysProTyrLeuPheSerValLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..TGCGGTGTGGCCCCCCAAGCA...CGCATCACAGGTGGCAGCAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee,J., Thompsho,P. and Lillle,J. Identification, assessment, prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 0118542-A 105 15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 1796)
e,J., Thompsho,P. and Lillie,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
599 c 511 g 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607.50
2.993
69.521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and therapy of ovarian
                                                        748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
                                                                                                                                                               869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr:BC001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             749
                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpValGluL
|||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTCCAAGAGGACATGGTGTGTGCTGGCTATGTGGAGGGGGCCAAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGCCTGGTGTACACTCTGGCCTCCAGCTATGCCTCCTGGATCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGluArgAs 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTGTAACTGCCTGTACAACATCGACGCCAAGCCTGAGGAGCCGCACTT 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAAGGTGACAGAACTCCAGCCTCGT 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysIleValGlnGlyValGlnLeuArg 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTACCTGACGGCATTGTGAGCTGGGGAGATGCCTGTGGGGCCCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGCCAGGGTGACTCTGGGGGGCCCACTCTCCTGCCCTGTGGAGGGTCTC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAspGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .IleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyGluArgAspA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Each eite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens, protease, serine, 8 IMAGE:3138532, mRNA, complete cds.
                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: nttp://lmaye.iiii.
Series: IRAL Plate: 4 Row: j Column: 3
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1809)
                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Collection (MGC), Cancer Ger
Institute, 31 Center Drive, Room
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC001462.1 GI:12655206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                               Zhang, L.-H. and Green, E.D.
                                                                                                                                      the following selection criteria: matched mRNA gi: 1143193 Location/Qualifiers
     /organism-"Homo sapiens"
/db_xref="LocusID:5652"
/db_xref="taxon:9606"
/clone="MGC:2133 IMAGE:3138532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1809 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 (prostasin),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11A03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone MGC:2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRI 12-JUL-2001
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: BC001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-040-803-7 x BC001462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ent Similarity:
140
                                                                                                                                                                                                                                                  535
                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                 485
                                                                                                                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                                                                                                               438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203
                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 laCysGlyLysProGlnGlnLeuAsnArgValValGlyGlyGluAspSer 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 uLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIleProValProProA 40
                                                                                                                                                               laAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSerGluArg 156
::|||||||||||:::::||| || || |||||:::
GCGACATTGCACTCCTCCAACTCAGCAGACCCATCACCTTCTCCCGCTAC 631
                                                                                                                                                                                                                                                                                                                                                                                                           ACTGCTTCCCCAGCGAGCACCACAAGGAA...GCCTATGAGGTCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThraspSerGluTrpProTrpIleValSerIleGlnLysasnGlyThrHi 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..TGCGGTGTGGCCCCCCAAGCA...CGCATCACAGGTGGCAGCAGTGCA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGlyGlyGlyCysLeuGlyThrPheThrSerLeuLeu.......
                                                                                ATCCGGCCCATCTGCCTCCCTGCAGCCCAACGCCTCCTTCCCCAACGGCCT
                                                                                                                                                                                                                                                  GAAGGACATCATCCCCCACCCCAGCTAC...CTCCAGGAGGGCTCCCAGG
                                                                                                                                                                                                                                                                       lAlaTrpValGluProHisProValTyrSerTrpLysGluGlyAlaCysA 140
                                                                                                                                                                                                                                                                                                                                                                   GlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLysValGlyVa 123
                                                                                                                                                                                                                                                                                                                                                                                                                                             isCysPheLysAspAsnLeuAsnLysProTyrLeuPheSerValLeuLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHisCysAlaGlySerLeuLeuThrSerArgTrpValIleThrAlaAlaH 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTCCGGTCGGGGACAGGAGCGGAAGGGGCAGAAGCTCCC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGGGCCTGGGCAGCTGGGGGGCCATTCTGCTCTATCTTGGATT 252
                                                                                                                       ValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAsnTh 173
                                                                                                                                                                                                                                                                                                                              GGGGCCCACCAGCTAGACTCCTACTCCGAGGACGCCAAGGTCAGCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="protease, serine, 8 (prostasin)"
/product="protease, serine, 8 (prostasin)"
/product="granal01462.1"
/protean_id="anal01462.1"
/db_xref="granal01462.1"
/db_xref="granal01462.1"
/db_xref="granal01462.1"
/db_xref="granal01462.1"
/db_xref="granal01462.1"
/db_xref="magkgvLopgQLGAVAILLYLGLLRSGTGAEGAEAPCGVAPQAR
ITGGSSAVAGQWPWQVSITYEGYHVCGGSLVSEQWVLSAAHCPSEPHHKEAYEVKLGA
HQLDSYSEDAKVSTLKDIIPHBSYLQEGSQGDIALLGLSRPITFSRYIHDAKPEEPHFVQ
EDMVCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASS
YASWIOSKYTELQPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSPWLSEH<sup>®</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: 185. .1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"__
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607.50
2.993
69.521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pote7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 7
Identity: 44.178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437
                                                                                                                                                                                                                                                    581
                                                                                                                                                                                                                                                                                                                                   534
                                                                                                                                                                                                                                                                                                                                                                                                                      484
                                                                                     681
```

```
1032 GCAAGGTGACAGAACTCCAGCCTCGT 1057
                                                                                                                                                                                                                            882 CCTGCCAGGGTGACTCTGGGGGGCCCACTCTCCTGCCCTGTGGAGGGTCTC
                                                                                                                                                                                                                                                                                                   190 roHisProGlnThrLeuGlnLysLeuLysValProIleIleAspSerGlu
|||::: |||||:::|||:::||||:::|||
732 TGACGCCCAAGCCACTGCAGCACTCGAGTGCCTCTGATCAGTCGTGAG
                                                                                              270 nArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpValGluL 287
                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                782
                                                                                                                                                                                                                                                                                                                                                                                                                 207 ValCysSerHisLeuTyrTrpArgGlyAla...GlyGlnGlyPro.....
                                                                                                                                                                       laCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAspGlyAla
                                 ysileValGlnGlyValGlnLeuArg 295
                                                                        CAGGCCTGGTGTACACTCTGGCCTCCAGCTATGCCTCCTGGATCCAAA 1031
                                                                                                                                                 TGGTACCTGACGGCATTGTGAGCTGGGGAGATGCCTGTGGGGCCCGCAA
                                                                                                                                                                                                                                                                                                                                                                                ACGTGTAACTGCCTGTACAACATCGACGCCAAGCCTGAGGAGCCGCACTT
                                                                                                                                                                                            270
                                                                                                                                                         981
                                                                                                                                                                                                                                  931
                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                             881
                                                                                                                                                                                                                                                                                                                                                237
                                                                                                                                                                                                                                                                                                                                                                                      831
                                                                                                                                                                                                                                                                                                                                                                                                                         220
```



```
Query length: 317
Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 210.970000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          About:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM of: US-10-040-803-7 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_l/USPf0_spocl/US10040803/runat_13082002_083353_7380/app_query.fasta_1.378
-Q=/cgn2_l/USPf0_spocl/US10040803/runat_13082002_083353_7380/app_query.fasta_1.378
-DB=u_Geneseq_032802 -OpwT-fastap -SUFFIX=p2n.rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=0.000 -VGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-PGAPOP=6.000 -GAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=Dlosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MIX=100 -THR_MIN=0 -ALIGN=10 -MODELCOAL -OUTFMT=pfs
-MCM=ext -HGAPSIZ=5500 -MINLEN=0 -MAXLEN=200000000
-NCM=CHAPSIZ=5500 -MINLEN=0 -MAXLEN=200000000
-NCM=CHAPSIZ=5500 -MINLEN=0 -MAXLEN=200000000
-NCM=0110040803_@CCN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
-THREADS=10 -MARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aug 13, 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Results were produced by the GenCore software, version 4. Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-040-803-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     out_format : pfs
                                                             1.6e-37
1.6e-37
2.6e-37
                                                                                                                           1.2e-47
3.1e-47
1.5e-46
                                                                                                                                                                                                                                  9.6e-92
4.6e-90
3.7e-88
6.0e-78
                                                                                                                                                                                                                                                                                                  4.4e-122
6.2e-116
3.4e-113
                                                                                                                                                                                                                                                                                                                                                                                    5.4e-123
5.4e-123
5.4e-123
                    4.4e-36
4.4e-36
                                                                                                                                                                                                                                                                                         2.1e-102
                                                                                                                                                                                                   1.4e-71
                                                                                                                                                                                                                                                                                                                                 5.4e-123
5.6e-123
5.7e-123
1.5e-122
1.5e-122
                                                                                                                                                                                                              8.8e-74
                                                                                                                                                         7.2e-48
7.4e-48
7.5e-48
8.0e-48
                                         8.5e-37
4.4e-36
                                                                                                       2.3e-43
4.7e-40
                                                                                                                                                                                                                          5.6e-75
                                                                                                                                                                                                                                                                               6.0e-102
                                                                                              3.4e - 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE XXX
            14 - AUG - 2000;

18 - AUG - 2000;

22 - AUG - 2000;

22 - AUG - 2000;

23 - AUG - 2000;

30 - AUG - 2000;

01 - SEP - 2000;
```

07-JUN-2000;

2000US-0198123. 2000US-0205515. 2000US-0209467. 2000US-0214886. 2000US-0215135. 2000US-0216647.

11-JUL-

2000US-0217487. 2000US-0217496.

2000US-0218290. 2000US-0220963.

14 - AUG

14 - AUG

14 - AUG 14 - AUG

2000US-022944
2000US-0224519
2000US-0224519
2000US-0225214
2000US-0225266
2000US-0225267
2000US-0225277
2000US-0225477
2000US-0225775
2000US-0225758
2000US-0225758
2000US-0225718
2000US-022579
2000US-022579
2000US-022579
2000US-022579
2000US-02258681
2000US-02258924
2000US-0229343
2000US-0229343
2000US-0229344
2000US-0229344

16-MAR-2000; 17-MAR-2000;

2000US-0186350. 2000US-0189874. 2000US-0190076.

2000US-0184664

18-APR-2000; .9-MAY-2000

02-MAR-2000;

17-JAN-2001;

2001WO-US01239

```
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF55267 + 581.00
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAC77814 + 576.50
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD03444 + 575.50
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:AAD23854 + 573.50
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD13117 + 554.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAS41085 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS41085
                                                                                                                                               Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                  cDNA encoding novel human enzyme polypeptide #301.
                                                                                                                        anti arthritic;
WO200155301-A2
                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS41085 standard; cDNA; 1352 BP
                                                                                                                     nephrotropic; anticoagulant; ss.
                                                                                                                                                                                                                                                                                        isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     791.20
781.73
779.47
773.29
747.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0e-34
) 2.9e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.5e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0e-35
```

```
\text{R} \text{ \text{C} \text{R} \text{ \text{C} \text{R} \text{C} \text{R} \text{C} \text{R} \text{C} \text{R} \text{R
                                              20-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

01-NOV-2000

08-NOV-2000

01-NOV-2000

01-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;

95-SEP-2000;

25-SEP-2000;

26-SEP-2000;

27-SEP-2000;

27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000;
12-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L4-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L4-SEP-2000;
                    2000US-0249208
2000US-0249209
2000US-0249210
2000US-0249211
2000US-0249211
2000US-0249212
2000US-0249213
2000US-0249213
2000US-0249215
                                                                                                                                                                                                                                             2000US-0241786.

2000US-02418787.

2000US-0241809.

2000US-02446174.

2000US-0246475.

2000US-0246476.

2000US-0246476.

2000US-0246478.

2000US-0246478.

2000US-0246523.

2000US-0246526.

2000US-0246526.

2000US-0246526.

2000US-0246526.

2000US-0246526.

2000US-0246526.

2000US-0246528.

2000US-0246528.

2000US-0246528.

2000US-0246539.

2000US-0246611.

2000US-0246611.

2000US-0246611.

2000US-0246611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0229513
2000US-0230438
2000US-0231242
2000US-0231242
2000US-0231241
2000US-02314113
2000US-02314114
2000US-0232081
2000US-0232081
2000US-0232081
2000US-0232399
2000US-0232399
2000US-0232399
2000US-0232401
2000US-0232401
2000US-0232401
2000US-0232401
2000US-0232401
2000US-0234241
2000US-0234241
2000US-0234249
2000US-0234249
2000US-0234299
2000US-0234299
2000US-0235484
2000US-0235834
2000US-0235836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0240960.
2000US-0241221.
2000US-0241785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0236802.
2000US-0237037.
2000US-0237038.
2000US-0237039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0237040.
2000US-0239935.
2000US-0239937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0236368.
2000US-0236369.
2000US-0236370.
```

```
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                     The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, the contraction of the invention are useful in the
                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                     diseases
                                                                                                                                                                                                                                                                                             pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                         Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reprodu
                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                 Rosen
                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                           2001-465566/50.
                                                                                                                                                                                                                                                             4; SEQ ID No 311; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0251989.
2000US-0251990.
2000US-0254097.
2000US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249217

2000US-0249218

2000US-0249245

2000US-0249264

2000US-0249264

2000US-0249267

2000US-0249267

2000US-0249297

2000US-0249390

2000US-0250160

2000US-0250160

2000US-0251981

2000US-0251988

2000US-0251868

2000US-0251868

2000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                 SM;
                                                                                                                                                                                                                                                                                                           reproductive,
```

isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. ALDS) autoimmune disorders (e.g. cancer), ce.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. hamphilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.

AAS40785-AAS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention.

Cancer of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification with the both and the concerns the sequence and the printed specification.

```
Sequence 1352 BP; 238 A; 446 C; 407 G; 261 T; 0 other;
```

```
alignment_block:
US-10-040-803-7
                                                                                                                                                alignment_scores:
                                       Align seg 1/1
                                                                                                        Ratio:
Percent Similarity:
1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyGlyCysLeuGlyTh 17
                                                                                                       Quality: 1720.00
Ratio: 5.426
milarity: 100.000
                                       ţo:
                                                                  ×
                                                                  AAS41085
                                       AAS41085
                                       from:
                                                                                                       Length: 317
Gaps: 0
Percent Identity: 100.000
                                       ç:
```

27 ATGGTGGTTTCTGGAGCGCCCCCAGCCCTGGGTGGGGGGCTGTCTCGGCAC 76

```
427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277
                                                                                                                                                                                                                  727
                                                                                                                                                                                                                                                                       677
                                                                                                                                                                                                                                                                                                217
                                                                                                                                                                                                                                                                                                                          627
                                                                                                                                                                                                                                                                                                                                        201 ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl
                                                                                                                                                                                                                                                                                                                                                                                577
                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                     527
                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                            301
                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal
                                                                                                                                                                                                                                                                                                                                                                                              lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTTCTCTGTGCTGGGGGGGCCCTGGCAGCTGGGGAACCCTGGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT
luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250
                                                                                                                                                                                                                                                                                                                             CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                AAGATGGAGTTCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACCTCCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCCAGAAGGTGGGTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                          CGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCGCACCGCTCCT
                                                                                                                        aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT
                                                                                                                                                                             AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCySAl
                                                                                                                                                                                                                   AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                                                                                     yGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG
                                                                                                                                                               GACGGCGCCTGGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
                                                                                                                                                                                                                                                                                                                                676
                                                                                                                                                                                                                                                                                                                                                        . 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426
                                                                                                                                                                                                                                                                                                                                                                                    626
                                                                                                              876
                                                                                                                                       284
                                                                                                                                                                   826
                                                          926
```

```
seq_documentation_block:
ID AAS26942 standard; cD
XX AAS26942;
XC AAS26942;
XT O7-NOV-2001 (first e
XX Human cDNA encoding a
XX Human; immunosuppress;
KW Human; immunosuppress;
KW Carebrovascular disord
KW Neuroprotective; anti
KW Cerebrovascular disord
KW Skin ageing; food add
XX Homo sapiens.
XX W0200155441-A2.
XX W0200155441-A2.
XX W0200155441-A2.
XX W0200155441-A2.
XX Homo sapiens.
XX Homo sapiens.
XX PPD 02-AUG-2001; 2000US-0PR 04-FEB-2000; 2000US-0PR 11-JUL-2000; 2000US-0PR 12-JUL-2000; 2000US-0PR 11-JUL-2000; 2000US-0PR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS26942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; hyperproviderative disorder; cerebral ischaemia; anglogenesis; nervous system disorder; cerebral ischaemia; anglogenesis; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        977 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding a novel secreted protein, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS26942 standard; cDNA; 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 r 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           977
     2000US-0214886.
2000US-0216647
2000US-0216647
2000US-0217487
2000US-0217487
2000US-0217487
2000US-021963
2000US-022964
2000US-02295114
2000US-0225214
2000US-0225266
2000US-0225266
2000US-0225266
2000US-0225266
2000US-0225277
2000US-0225447
2000US-0225477
2000US-0225758
2000US-02258681
2000US-02258924
2000US-02258924
2000US-0229343
2000US-0229343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US01320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0209467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-02055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0198123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0190076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0189874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0184664.
2000US-0186350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0179065
```

```
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                              20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                          20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                            14 - SEP - 2000;
21 - SEP - 2000;
21 - SEP - 2000;
25 - SEP - 2000;
25 - SEP - 2000;
26 - SEP - 2000;
27 - SEP - 2000;
27 - SEP - 2000;
29 - SEP - 2000;
20 - CCT - 2000;
                                    17-NOV-2000;
                                               17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000;
02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                     02-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                            13-0CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2000;
             2000US-0234223
2000US-0234998
2000US-0235884
2000US-0235884
2000US-0235884
2000US-0235886
2000US-0236368
2000US-0236368
2000US-0236368
2000US-0236369
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0241787
2000US-024677
2000US-024677
2000US-024677
2000US-024677
2000US-024677
2000US-024677
2000US-024677
2000US-024677
2000US-0246528
2000US-0246528
2000US-0246528
2000US-0246528
2000US-0246528
2000US-0246511
2000US-0246511
2000US-0249211
2000US-0249211
2000US-0249211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0232080
2000US-0232081
2000US-0231968
2000US-0231968
2000US-0232397
2000US-0232398
2000US-0232399
2000US-0232401
2000US-0232401
2000US-0233403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0231244.
2000US-0231413.
2000US-0231414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0229509.
2000US-0229513.
2000US-0230437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0233064.
2000US-0233065.
```

```
The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC arabits, goats, horses, cats, dogs, chickens or sheep. They can also used in diagnosing a pathological condition or susceptibility CC to a pathological condition. Antibodies to the proteins can also CC include autoimmunoassays e.g. radioimmunoassays or enzyme linked CC include autoimmune diseases e.g. rheumatoid arrhitis, CC hyperproliferative disorders e.g. neoplasms of the breast or liver, CC traftovascular disorders e.g. cardiac arrest, cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungicand coular disorders e.g. corneal infection, and many other CC disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before
transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 134; 601pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-476222/51.
P-PSDB; AAU17037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249300

2000US-0250391

2000US-02519391

2000US-0251938

2000US-0251798

2000US-025179

2000US-0251856

2000US-0251868

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0249264.
2000US-0249265.
2000US-0249297.
2000US-0249299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0249218.
2000US-0249244.
2000US-0249245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0249216.
2000US-0249217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
```

alignment_block: US-10-040-803-7

x AAS26942

Percent Similarity:

5.426 100.000

Length: 317
Gaps: 0
Percent Identity: 100.000

Align seg 1/1 to: AAS26942

1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh 17

from: 1

to: 1352

alignment_scores:

Quality: 1720.00 Ratio: 5.426

```
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                       827
                                                                                                                                                                                                                                                                 677
                                                                                                                                                                                                                                                                                                                          627
                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                    577
                                                                                                                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                               777
                                                                                                                                                                                                       727
                                                                                                                                                                                                                                    234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                         284
                                                                                                                 267
301 GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaArgSe 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpVallleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rqIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                             AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl
                                                                                                                                                                                                                     luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250
                                                                                                                                                                                                                                                                                                                                        ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl 217
                                                                                                                                                                                                                                                                                                                                                                                                  lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                             rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly 300
                                                                                                     aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT 284
                                                                                                                                               yGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG
                                                                                                                                                                                                                                                                                                                                                                                    AAGATGGAGTTCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT 626
                                                                                                                                                                                                                                                                                                                                                                                                                                             eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT 526
                             GGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGGGG
                                                                                    CGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCGCACCGCTCCT 876
                                                                                                                                                                                                     AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                                                                                 ACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTTGGAGGGGG
                                                                                                                                                                                                                                                                                                                          CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76
                                                                                                                                                                                                                                                                                                 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476
                                                                                                                                                  826
                                                                                                                                                                            267
                                                                                                                                                                                                                                                                    726
                                                                                                                                                                                                                                                                                                                             676
                                  926
                                                                                                                                                                                                            776
```

alignment_scores

```
seq_name:
                       This is the nucleotide sequence of cDNA clone DNA43318 (ATCC 209481) coding for human PRO343 (UNQ302) (see AAY06482). The clone was sisolated from a foetal lung library. Amplification of DNA43318 (chromosome 16) was observed in primary lung and primary colon tumours, suggesting an association with tumour formation or growth. Antagonists (e.g. antibodies) directed against PRO343 may have utility in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded the gene hav06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may call as a predictors of the prognosis of tumour treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           977 C 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 r 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO343; UNQ302; cancer; tumour; diagnosis; therapy; human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA clone encoding human PRO343, amplified in tumour cells.
                                                                                                                                                                                                                                                Antibody against proteins expressed in neoplastic cells, useful for
                                                                                                                                                                                                            Example 1; Fig 11; 162pp; English.
                                                                                                                                                                                                                                     tumor diagnosis and treatment
                                                                                                                                                                                                                                                                                         WPI; 1999-430385/36
                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX87259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                 Goddard
                                                                                                                                                                                                                                                                                                                                                                                                98US-0070440.
98US-0083500.
98US-0086414.
98US-0088742.
                                                                                                                                                                                                                                                                                                                                                                                   98US-0107783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= 6
53..148
                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0109304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US00106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
149..1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53..1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'ocation/Qualifiers
     235 A; 461 C; 412 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA; 1378 BP
                                                                                                                                                                                                                                                                                                                                 ۶
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          עם
                                                                                                                                                                                                                                                                                                                                   Gurney AL,
                                                                                                                                                                                                                                                                                                                                   Hillan
        270 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    ΚJ,
                                                                                                                                                                                                                                                                                                                                    Lawrence
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAX87259 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-040-803-7 x AAX87259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity: 100.000
                                                              234 luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250
                                                                                                       703
                                                                                                                               217
                                                                                                                                                        653
                                                                                                                                                                                                          603
                           251
                                                                                                                                                                                                                                 184
                                                                                                                                                                                201
                                                                                                                                                                                                                                                           553
                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                             453
                                                                                                                                                                                                                                                                                                                                                                                                              403
                                                                                                                                                                                                                                                                                                           503
                                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                                                                              353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153
                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASPG1yAlaTrpLeuLeuAlaG1yIleIleSerTrpG1yG1uG1yCysAl
                                                                                                 GACGGCGCCTGGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGC
                                                                                                                                                  CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGG
                                                                                                                                                               ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl
                                                                                                                                                                                                                lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal
                                                                                                                                                                                                                                                                   eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG
                                                                                                                                                                                                                                                                                                                                                                                                      AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                    AAGATGGAGTTCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT
                                                                                                                                                                                                                                                                                                                    IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT
                                                                                                                                                                                                                                                                                                                                                        GAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC
                                                                                                                                                                                                                                                                                                                                                                        rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA 34
                                                                                                                                                                                                                                                     CCACCTCCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTTCTCTGTGCTGCGGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCACCTCCCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 1720.00
Ratio: 5.426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317
852
                                                                                                                                                                           217
                       267
                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                                                                                                                                                                          402
                                                 802
                                                                                                   752
                                                                                                                           234
                                                                                                                                                                                                    652
                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                     602
                                                                                                                                                                                                                                                                             184
                                                                                                                                                   702
                                                                                                                                                                                                                                                                                                       552
                                                                                                                                                                                                                                                                                                                                                         502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
```

```
seq_documentation_block:
ID AAX52262 standard; DNA; 1378 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX52262
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
29-OCT-1997;
                                                                    18-SEP-1997
18-SEP-1997
15-OCT-1997
17-OCT-1997
17-OCT-1997
21-OCT-1997
24-OCT-1997
26-OCT-1997
                                                                                                                                                                                                                                                                                                              25-NOV-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; transmembrane protein; human; enterocolitis; collinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1003 C 1003
                                                                                                                                                                                                                                                                                      17-SEP-1997
17-SEP-1997
                                                                                                                                                                                                                                                               17-SEP-1997
                                                                                                                                                                                                                                                                            17-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853
                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9914328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein PRO343 cDNA clone DNA43318-1217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCCTCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCGCACCGCTCCT
                    970S-0063329
970S-0063327
970S-0063541
970S-0063542
970S-0063544
970S-0063549
970S-0063550
                                                                                                       970S-0062285.
970S-0062287.
970S-0062814.
970S-0062814.
970S-0062816.
970S-0063120.
970S-0063120.
970S-0063127.
970S-0063128.
                                                                                                                                                                                                                            97US-0059121.
97US-0059122.
97US-0059184.
97US-0059263.
97US-0059266.
97US-0062125.
                                                                                                                                                                                                                                                                                                  97us-0059119
                                                                                                                                                                                                                                                                                                                        97US-0059113
97US-0059115
                                                                                                                                                                                                                                                                                                              97US-0059117
                                                                                                                                                                                                                                                                                                                                                                        98WO-US19330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
```

```
8288888
                                                                                                                             alignment_block:
                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                         Quality: 1720.00
Ratio: 5.426
Percent Similarity: 100.000
                                                                     Align seg 1/1 to: AAX52262
                                                                                                            US-10-040-803-7 x AAX52262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1997;
29-OCT-1997;
31-OCT-1997;
31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                               Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease Alzheimer's disease, ALS, neuropathies or cancer. PROZ65 can be used as for fibromodulin, e.g. for reducing dermal scarring. PROZ64 can be used as a target for anti-tumor drugs. PROZ63 may be used in the treatment of Usher Syndrome or Atrophia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO217 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. entercoolitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-1997;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1997;
                                                                                                                                                                                                                                                                                                                             areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 97; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-229533/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and polypeptides used in, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                           Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                            in the heart of genital tract.
53 ATGGTGGTTTCTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCAC 102
                     -NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9703-0064103
9703-0064248
9703-0065186
9703-0065186
9703-0065186
9703-0065120
9703-0066120
9703-0066772
9703-0066772
9703-0066711
9703-0066511
9703-006651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0064215.
97US-0063735.
97US-0063870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0063704.
97US-0063732.
97US-0063738.
                                                                         from: 1 to: 1378
                                                                                                                                                                Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood WI,
```

17 rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA 34

317 r 317

```
453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553
                                                                                                                                                                                                                                                                                            234 luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal
                                                                                                                                                                                                                                                                                                                                                                             217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal 50
903
                                                                                      284 rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCACCTCCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTTCTCTGTGCTGCGGGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                            ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                        AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaArgSe
                                                                                                                                                       aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT
                                                                                                                                                                                                                                                                                                                                                             CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGG
                                                                      GGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGGGG
                                                                                                                                      CGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCGCACCGCTCCT
                                                                                                                                                                                                           GACGGCGCCTGGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGC
                                                                                                                                                                                                                                                                          AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                                                                                                                                                            ACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTTGGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
        1002
                                                                                                                                                                                                                                                                                                                 250
                                                                                                                                                                                                                                                                                                                                                                                                                    702
                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552
                                                                                                                                              902
                                                                                                                                                                              284
                                                                                                                                                                                                                                               267
                                                                                                                                                                                                                                                                                                                                                  752
                                                                                                                                                                                                                                                                                                                                                                                  234
```

1003 C 1003

```
seq_documentation_block:
ID AAA46914 standard; cD
XX
AC AAA46914;
XX
DT 03-OCT-2000 (first e
XX
CDNA encoding novel p
XX
PRO201; PRO292; PRO32
KW PRO2015; PRO1017; PRO1
KW tumourigenesis; cance
XX
XX
EH Key Locat
alignment_block:
US-10-040-803-7 x AAA46914
                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1720.00
Ratio: 5.426
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA46914
                                                                                                                                                                                 The present sequence encodes a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO314, PRO343, PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and are useful in the treatment and diagnosis of neoplastic cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1998;
08-MAR-1999;
02-JUN-1999;
01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
                                                                                                                                       Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 other;
                                                                                                                                                             and proliferation in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-452188/39.
P-PSDB; AAY93689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                      New anti-polypeptide antibody useful in the treatment and diagnosis eoplastic ceil growth and proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botstein D, Goddard A, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                        Claim 50; Fig 11; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200037640-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding novel polypeptide PRO343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA46914 standard; cDNA; 1378 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0113296.
99WO-US12525.
99WO-US12752.
99WO-US20111.
99WO-US21090.
99WO-US21090.
99WO-US21090.
99WO-US21090.
99WO-US21090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US30095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 53..1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney AL,
                                              Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillan K,
                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                   of.
```

```
Align seg 1/1 to: AAA46914 from: 1 to: 1378
```

	o G	n 0 1	234 753	217 703	201 653	184 603	167 553	151 503	134 453	117 403	101 353	84 303	67 253	51 203	34 153	17 103	53 1	1gn s
			.uArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 2	yGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG 234 	ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl 217 	lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200 	eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184	IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167 	rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 15(gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134 	LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117 	rpVallleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100 	eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT 84 	ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67	rglleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal 50	rPheThrSerLeuLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA 34	MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh 17 	seg 1/1 to: AAA46914 from: 1 to: 1378
										- /					2	N	₽	

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF72420
                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block: ID AAF72420 standard.
  Ashkeuu...
Filvaroff E, Fony U
Godowski PJ, Grimal
Godowski PJ, Pan J,
                                                                                                                                                                                                                                                                                                            15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
16-DEC-1999;
20-DEC-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF72420 standard; cDNA; 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200104311-A1
The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g.
                                                                                                        Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001
                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ischaemia; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        luman PRO343 cDNA
                                                                                              Alzheimer's disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                     L3-SEP-1999;
                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r 317
                                                                                                                                                                             2001-081051/09.
                                                                                                                                                               AAB80259
                                                                                                                                                                                                      PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; antipsoriatic; cytostatic; antiinflammatory;
                                                                  97; 393pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US04414.
                                                                                                                                                                                                                   Botstein D, Desnoyers L,
Fong S, Gao W, Gerber H,
Grimaldi CJ, Gurney AL, E
Van J, Paoni NF, Roy MA, S
                                                                                                                                                                                                      Wood WI;
                                                                                                                                                                                                                                                                                                               99WO-US30991.
99WO-US30999.
99WO-US00219.
                                                                                                                                                                                                                                                                                                                                                     99WO-US28214.
99WO-US28313.
99WO-US30095.
                                                                                                                                                                                                                                                                                                                                                                                                                       99W0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0145698
99US-0146222
                                                                                                                                                                                                                                                                                                                                                                                            99WO-US21547
99WO-US23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0143048
                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US20944
                                                                                                                                                                                                                                                                                                                                                                                                                        ·US21090.
                                                                     English
                                                                                                                                                                                                                   L, Eaton DL,
H, Gerritsen I
Hillan KJ, I
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal disorder;
                                                                                                                                                                                                                                               Œ,
                                                                                                                                                                                                                                    Kljavin
                                                                                                                                                                                                                                                            Ferrara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                 Goddard
                  (e.g. lung
                                                                                                                                                                                                                                                 A;
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAF72420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-040-803-7 x AAF72420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including the PRO nucleic acids have applications in molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use as hybridization probes, and in chromosome and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
                                                                                                  184
                                                                                                                                                                                                   503
                                                                                                                                                                                                                                                                    453
                                                                                                                                                                                                                                                                                     134 rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer
                                                                                                                                                                                                                                                                                                                                      403
                                                                                                                                                                                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                     101 LeuPhcSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGTGGTTTCTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpvallleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT
lnAspGlyValProLeuProHisProGlnThrLeuGlnLysUeuLysVal
                                                                                                                                IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl
                                                                                                                                                                                                                                                                                                                                                      AAGATGGAGTTCCCTTGCCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT
                                                                                                                                                                                                   ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT
                                                                                                                                                                                                                                                                    GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC
                                                                                                                                                                                                                                                                                                                                      GTCCCAGAAGGTGGGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 1720.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.000
                                        217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
                                                                                                                                                                                                                                                                                                                                            452
                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                             402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352
                                                                         652
                                                                                                                                         602
                                                                                                                                                                        184
                                                                                                                                                                                                                                                                                                        150
```

```
seq_documentation_block:
ID AAD02990 standard; cD
XX
AAD02990;
XX
DT 31-MAY-2001 (first e
XX
DT 31-MAY-2001 protease
XX
Human serine protease
XX
Human; serine proteas
XX
I aundry detergent; sh
KW neurodegenerative dis
XX
OS Homo sapiens.
XX
OS Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD02990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1003 C 1003
                              Novel serine protease termed protease C-E, useful for treating preventing skin flaking or imbalance of desquamation \boldsymbol{\cdot}
     Claim 2;
                                                                                                       WPI; 2001-226681/23.
                                                                                                                                        Darrow A, Qi J, Andrade-Gordon
                                                                                           P-PSDB; AAY72890.
                                                                                                                                                                                                                 31-AUG-1999;
                                                                                                                                                                                                                                                14-AUG-2000;
                                                                                                                                                                                                                                                                                     08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; serine protease; protease C-E; therapy; desquamation; skin care; laundry detergent; shampoo; cleaning agent; hair care; skin flaking; neurodegenerative disorder; dermatological; immunogenic; proteolytic;
                                                                                                                                                                           (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                       WO200116288-A2
                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome 16p13.3; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human serine protease, protease C-E cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 r 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaArgSe 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD02990 standard; cDNA; 1430 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpValGluLysI1eValGlnGlyValGlnLeuArgGlyArgAlaGlnGly 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGGGATGCTTGTGTGGGCGACTCCGGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250
Fig 1; 78pp;
                                                                                                                                                                                                                                                2000WO-US22117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                               99US-0386629.
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 113..1066
                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Human serine protease, protease C-E"
 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
```

The present sequence is a human serine protease, protease

G-E

cDNA which

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9999999999998<del>%</del>&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 1720.00
Ratio: 5.426
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAD02990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-040-803-7 x AAD02990
                    184 lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal
                                                                                                                                                                                                                                                                                                                                                       463
                                                                                                                                                                                              151 IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerI1 167
                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                           413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is a member of the S1 serine protease family. Protease C-E gene is located on chromosome 16p13.3 and is expressed in pancreas, placenta, prostate, small intestine, stomach, spleen, fibroblasts, epidermis, cerebellum, cerebral cortex, pituitary and hippocampus. Protease C-E is useful for treating an imbalance of desquamation, by topical application. A non-pharmaceutical composition comprising the protein may be formulated as a laundry detergent, shampoo, hard surface cleaning composition, dish care cleaning composition, skin care composition and hair care composition. Protease C-E is useful for treating and preventing skin flaking, neurodegenerative disorders and dermatological pathologies. It is less immunogenic to sensitive individuals and it provides efficient proteolytic activity in a non-natural environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 CTTCACCTCCCTGCTGCTGCTGCGTCGACAGCCATCCTCAATGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 ATGGTGGTTTCTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1430 BP; 240 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyGlyCysLeuGlyTh
AAGATGGAGTTCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT
                                                                                                          eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG
                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACCTCCCTCCAAACACCCCACTGCTGGATCTCAGGCTGGGGGAGCATCC
                                                                                                                                                                            ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT
                                                                                                                                                                                                                                                              GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC
                                                                                                                                                                                                                                                                                       rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                         gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                  GTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTGATCACTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 C; 428 G; 278 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                    662
                                                                                                                               184
                                                                                                                                                                        612
                                                                                                                                                                                                                                                              562
                                                                                                                                                                                                                                                                                                                                                                                                                                      462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212
```

```
seq_documentation_block:
ID AAS26871 standard; cDNA; 1439 BP
XX
AC AAS26871;
XX
DT 07-NOV-2001 (first entry)
XX
DT U7-NOV-2001 (first entry)
XX
BT WHuman cDNA encoding a novel secr
XX
KW Human; immunosuppressive; antiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

16-MAR-2000

17-MAR-2000

18-AFR-2000

19-MAY-2000

07-JUN-2000

28-JUN-2000

30-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1063 C 1063
                                                                                                                                                                                                                                                                                                                                                                       cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fingicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; nervous system disorder; cerebral ischaemia; anglogenesis; nervous system disorder; cerebral ischaemia; anglogenesis; corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immunosuppressive; antiarthritic; ss; antirheumatic;
                                                                                                                                                                                                                17-JAN-2001;
                                                                                                                                                                                                                                                                                  WO200155441-A2
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA encoding a novel secreted protein, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTTGGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS26871
2000US-0179065.

2000US-0180628.

2000US-0184664.

2000US-0186350.

2000US-0198774.

2000US-0198173.

2000US-0198173.

2000US-0205515.

2000US-020467.

2000US-0214886.

2000US-0214886.
                                                                                                                                                                                                              2001WO-US01320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
     07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
14-AUG-2000)
12-AUG-2000)
22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
23-AUG-2000)
01-SEP-2000)
01-SEP-2000]
                  08-SEP-2000
18-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
11-SEP-2000
21-SEP-2000
21-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
21-SEP-2000
29-SEP-2000
21-SEP-2000
21-SEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0216647.
2000US-0216880.
2000US-0217487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0228924.

2000US-0229287.

2000US-0229343.

2000US-0229344.

2000US-0229345.

2000US-0229345.

2000US-0229513.

2000US-0229513.

2000US-0239533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0226681.
2000US-0226868.
2000US-0227182.
2000US-0227009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0225758.
2000US-0225759.
2000US-0226279.
   2000US-0237040
2000US-023935,
2000US-0239937,
2000US-0240960,
2000US-0241221,
2000US-0241786,
2000US-0241786,
2000US-0241787,
                                                                                                                                                                                                                                                                                                                                                       2000US-0233065.
2000US-0234223.
2000US-0234274.
2000US-0234997.
2000US-0234998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0232397.
2000US-0232398.
2000US-0232399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0230438.
2000US-0231242.
2000US-0231243.
2000US-0231244.
                                                                                                                                                                                                                                 2000US-0236368.
2000US-0236369.
                                                                                                                                                                                                                                                                                    2000US-0235836
2000US-0236327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0232080.
2000US-0232081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0225757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0225447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0225268
2000US-0225270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0225266
2000US-0225267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0225214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0225213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0224519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0220964
2000US-0224518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0218290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0217496
                                                                                                                                                            2000US-0237037
2000US-0237038
                                                                                                                                                                                                                                                                                                                       2000US-0235484.
2000US-0235834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0233064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0232400.
2000US-0232401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0231414
                                                                                                                                              2000US-0237039
                                                                                                                                                                                                 2000US-0236802.
                                                                                                                                                                                                                    2000US-0236370
                                                                                                                                                                                                                                                                  2000US-0236367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0233063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0231968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0231413.
```

```
20-CCT-2000
20-CCT-2000
20-CCT-2000
01-NOV-2000
08-NOV-2000
                                                                                                                                                                                                                                                                                                       17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                      2000US-0241808.
2000US-0241808.
2000US-0241809.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246524.
2000US-0246525.
2000US-0246526.
2000US-0246527.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0249207.
2000US-0249217.
2000US-0249217.
2000US-0249217.
2000US-0249218.
2000US-0249219.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249219.
2000US-02511868.
2000US-0251189.
2000US-0251199.
2000US-02540978.
```

HUMA-) HUMAN GENOME SCI INC.

Barash SC, Ruben MS.

P-PSDB; 2001-476222/51. AAU16966.

diagnose diseases or disorders associated with aberrar activity of polypeptides, for treating blood clotting haemophilia Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or disorder, or ç

Claim 1; SEQ ID No 63; 601pp; English.

encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility are also used in diagnosing a pathological condition or susceptibility. The invention relates to isolated nucleic acid molecules and their a ç the proteins susceptibility

alignment_scores:
 Quality: alignment_block: US-10-040-803-7 x AAS26871 Align seg 1/1 to: AAS26871 Percent Similarity: Alzhelmer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. 454 117 404 304 504 134 354 154 101 254 204 104 ATGGTGGTTTCTGGAGCGCCCCCAGCCCTGGGTGGGGGGCTGTCTCGGCAC 84 67 51 34 17 rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal CTTCACCTCCTGCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCA rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG GTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT CTGTTCTCTGTGCTGGGGGGGGCCTGGCAGCTGGGAACCCTGGCTCTCG CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT CCACCTCCCTAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCC ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT Ratio: 5.426 100.000 1720.00 from: 1 Gaps: 0
Percent Identity: 100.000 to: 1439 Length: 200 653 184 603 167 453 403 100 353 84 303 67 203 153

```
seq_documentation_block:
ID AAS41621 standard; cDNA; 1352 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS41621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1054 C 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217
31-JAN-2000;
04-EEB-2000;
24-EEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAY-2000;
11-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase)ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding novel human enzyme polypeptide #837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317
                                                                                                                                                                                                                                                                                                                                                                                 anti arthritic; nephrotropic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                     blood-related disorder; infectious disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                     17-JAN-2001;
                                                                                                                                                                                                                                                                          02-AUG-2001.
                                                                                                                                                                                                                                                                                                            WO200155301-A2
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaArgSe 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGGCGCCTGGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCCTCATGTGCCAGGTG
 2000US-0119065.
2000US-01184664.
2000US-01184664.
2000US-01186350.
2000US-01189874.
2000US-01198123.
2000US-0205515.
2000US-020467.
2000US-02148647.
2000US-0216647.
                                                                                                                                                                                                                                       2001WO-US01239.
                                                                                                                                                                                                                                                                                                                                                                                     gene
ss.
                                                                                                                                                                                                                                                                                                                                                                                                      therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isomerase;
         14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
12-AUG-2000;
12-AUG-2000;
13-AUG-2000;
14-AUG-2000;
13-AUG-2000;
14-AUG-2000;
16-SEP-2000;
17-SEP-2000;
18-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
         14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
21-CCT-2000;
20-CCT-2000;
21-CCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0216880

2000US-0217487

2000US-0217496

2000US-0218290

2000US-022963

2000US-022964

2000US-0224518

2000US-0224518

2000US-0225214

2000US-0225214

2000US-0225266

2000US-0225266

2000US-0225268

2000US-0225268

2000US-0225270

2000US-0225277

2000US-0225477

2000US-0225477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0231414.
2000US-0232080.
2000US-0232081.
2000US-0232081.
2000US-0231968.
2000US-0232397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0229345
2000US-0229509
2000US-0229513
2000US-0239437
2000US-0230438
2000US-0231242
2000US-0231242
2000US-0231244
                                                                                                                                                                                                                                                                                                                                                        2000US-0233065.
2000US-0234223.
2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
2000US-0235834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0232398.
2000US-0232399.
2000US-0232400.
2000US-0232401.
2000US-0233063.
2000US-0233064.
           2000US-0237040.

2000US-0239935.

2000US-0239937.

2000US-0240960.

2000US-0241721.

2000US-0241786.

2000US-0241787.

2000US-0241787.

2000US-0241787.
                                                                                                                                                                                                           2000US-0236367
2000US-0236368
2000US-0236369
2000US-0236370
2000US-0236802
2000US-0237037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0225759
2000US-0226279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0229343
2000US-0229344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0228924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0226868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0226681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0225758
                                                                                                                                                                            2000US-0237038.
2000US-0237039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0231413
                                                                                                                                                                                                                                                                                                                      2000US-0235836.
2000US-0236327.
```

ZXZXEX X

```
The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of
                                                                                                                                                                                                                                                                                                                         08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
diagnosis, treatment, prevention and the first (e.g. cancer), disorders including hyperproliferative disorders (e.g. cancer),
                                                                                                                                       Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous pulmonary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                           WPI; 2001-465566/50.
P-PSDB; AAU23751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                       Claim 4; SEQ ID No 847; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2000;
                                                                                                                                                                                                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                              2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0241809
2000US-0244617
2000US-0246474
2000US-0246475
2000US-0246478
2000US-0246478
2000US-0246524
2000US-0246524
2000US-0246524
2000US-0246528
2000US-0246528
2000US-0246528
2000US-0246610
2000US-0246611
2000US-0246611
2000US-0249201
2000US-0249201
2000US-0249201
2000US-0249211
2000US-0249211
                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249295.
2000US-0249299.
2000US-0249299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0249217.
2000US-0249218.
2000US-0249244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0249214.
2000US-0249215.
2000US-0249216.
                                                                                                                                                                                                                                                                                       2000US-0251990
2000US-0254097
                                                                                                                                                                                                                                                                                                              2000US-0251989
                                                                                                                                                                                                                                                                                                                         2000US-0251869
                                                                                                                                                                                                                                                                                                                                     2000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                              2000US-0250391.
2000US-0251030.
                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0250160.
                                                                                                                                                                                                                                                    SCI INC
```

```
alignment_block:
US-10-040-803-7 x AAS41621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               999999999999888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAS41621 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                        467
                                                                                                                                                                                                                                                          417
                                                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                           367
                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAS40785-AAS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1352 BP; 237 A; 444 C; 408 G; 260 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 ATGGTGGTTTCTGGAGCGCCCCAGCCCTGGGTGGGGGGCTGTCTCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh 17
lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal
                                                                                                                                                                                        IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerI1
                                                                                                         eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG
                                                                                                                                                                                                                                                                         rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT
                                                                                 CCACCTCCCTCCAAACACCCCACTGCTGGATCTCAGGCTGGGGGAGCATCC
                                                                                                                                                                  ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT
                                                                                                                                                                                                                                                     GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC
                                                                                                                                                                                                                                                                                                                                    GTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT
                                                                                                                                                                                                                                                                                                                                                                            gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT
                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTTCTCTGTGCTGGGGGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTGATCACTGCCGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAKAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValGlyGlyGluAspSerThrAspSerGluTrpProTrpI1eValSerI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCACCTCCCTGCTGCTGCCGCCGTCKACAGCCATCCTCAATGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1714.00
5.424
99.685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 99.685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1352
616
                                         200
                                                                                   566
                                                                                                                          184
                                                                                                                                                                    516
                                                                                                                                                                                                                                                   466
                                                                                                                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
```

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS26943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID AAS26943 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                               Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; nervous system disorder; cerebral ischaemla; anglogenesis; nervous system disorder; cerebral ischaemla; nection; ocular disorder; corneal infection; wound healing; epithelial cell proliferative. skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      β17
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding a novel secreted protein, SEQ ID 135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS26943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS26943 standard; cDNA; 1352 BP
                                                                                                                                                                                                              02-AUG-2001
                                                                                                                                                                                                                                             WO200155441-A2
                                                                                                                                                                                  17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCGCCGCGCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaAlaArgSe 317
                                                                                                     2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0199874.
2000US-0199076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215135.
                                                                                                                                                                                   2001WO-US01320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         966
         14-AUG-2000)
11-AUG-2000)
11-AUG-2000)
22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
23-AUG-2000)
23-AUG-2000)
01-SEP-2000)
01-SEP-2000]
       14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
21-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0229343.
2000US-0229344.
2000US-0229345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0225758.
2000US-0225759.
2000US-0226279.
2000US-0226681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0225270.
2000US-0225447.
2000US-0225757.
         2000US-0234084
2000US-0234085
2000US-0234274
2000US-0234274
2000US-0234997
2000US-0235836
2000US-0235836
2000US-0235836
2000US-0235836
2000US-0236367
2000US-0236369
2000US-0236369
2000US-0236369
2000US-0236370
2000US-0236370
2000US-0237037
2000US-023703937
2000US-023703937
2000US-02347186
2000US-0244786
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0231968.
2000US-0232397.
2000US-0232398.
2000US-0232399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0224519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0224518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0225266
2000US-0225267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0228924.
2000US-0229287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0227009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0225268
                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0232400.
2000US-0232401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0231413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0231242.
2000US-0231243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0230438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0230437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0229513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0227182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0226868.
                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0233063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0232080.
2000US-0232081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0231414.
```

```
PR
PR
PR
PR
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                          08-DEC-2000;
                                                                                                                                                                                                                                 05-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                          06-DEC-2000;
                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                17-NOV-2000;
                                                                                                                                                                                                                                                                                                       17-NOV-2000;
                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NOV-2000;
                                                                                                                                                                                             2000US-0251856.
2000US-0251868.
2000US-0251869.
                                                                                                                                                                                                                                                                                                                            2000US-0246528.
2000US-0246529.
2000US-0246532.
2000US-0246609.
2000US-0246611.
2000US-0249207.
2000US-0249207.
2000US-0249210.
2000US-0249211.
2000US-0249212.
2000US-0249213.
2000US-0249213.
2000US-0249213.
2000US-0249214.
2000US-0249215.
2000US-0249216.
2000US-0249216.
2000US-0249218.
                                                                                                                                                                                                                                                                             2000US-0249244.

2000US-0249245.

2000US-0249264.

2000US-0249265.

2000US-0249297.

2000US-0249299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000US-0241808.
; 2000US-0241809.
; 2000US-0244817.
; 2000US-0246474.
; 2000US-0246475.
; 2000US-0246476.
; 2000US-0246476.
; 2000US-0246478.
                                                                                                                                                                          2000US-0251990.
2000US-0254097.
                                                                                                                                                                                          2000US-0251989
                                                                                                                                                                                                                        2000US-0251479.
                                                                                                                                                                                                                                                2000US-0251030.
                                                                                                                                                                                                                                                        2000US-0250160.
2000US-0250391.
                                                                                                                                                                                                                                                                       2000US-0249300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0246523.
2000US-0246524.
2000US-0246525.
```

(HUMA-) HUMAN GENOME SCI INC

Barash SC, SM;

P-PSDB; AAU17038. 2001-476222/51.

Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, harmonists. haemophilia ç

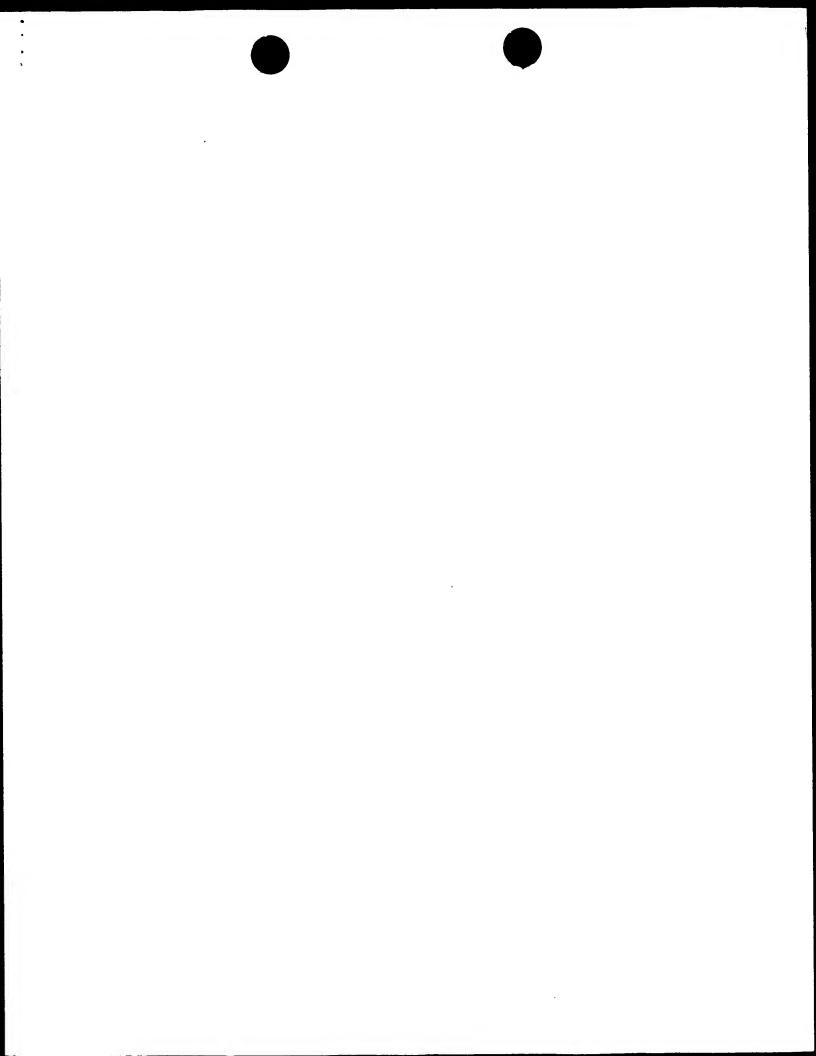
Claim 1; SEQ ID No 135; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility pathological condition. Antibodies to the proteins can also

184 lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200

aliqnment_block: alignment_scores: 8888888888888888888 be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated conclude autoimmune diseases e.g. rheumatoid arthritis, conclude autoimmune diseases e.g. neoplasms of the breast or liver, conclude autoimmune diseases e.g. neoplasms of the breast or liver, conclude autoimmune diseases e.g. neoplasms of the breast or liver, conclude autoimmune diseases e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, versebrovascular disorders e.g. cardiac arrest, versebrovascular disorders e.g. and ocular disorders e.g. corneal infection, and many other condition of the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to conclude the sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to cregenerate tissues and in chemotaxis. The polypeptides can also be used cas a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, and the prosecute of the process. Align seg 1/1 to: AAS26943 US-10-040-803-7 x AAS26943 Percent Similarity: 151 417 367 134 117 101 267 217 167 117 GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT 84 67 51 ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 34 rg|leProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal 17 eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG ATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTAT IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT LeuPheSerValLeuGuyAlaTrpGlnLeuGlyAsnProGlySerAr rpVallleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100 CCAKAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC GTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT CTGTTCTCTGTGCTGGGGGGGCCTGGCAGCTGGGAACCCTGGCTCTCG GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT Quality: Ratio: cofactors and other nutritional components. The present 1714.00 5.424 99.685 from: Gaps: 0
Percent Identity: 99.685 to: 1352 Length: 184 466 266 84 216 67 166 50 116

		\ \		,				
317 967	301 917	284 867	267 817	251 767	234 717	217 667	201 617	567
r 317 C 967			aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT 284	ASPG1yAlaTrpLeuLeuAlaG1yIleIleSerTrpG1yG1uG1yCysA1 267	luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250	yGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG 234 	ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl 217	



```
gb_est2:BI218460
gb_est2:BI763558
gb_est2:BF789214
gb_est1:AW383305
gb_est2:BG969117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est1:AW462598
gb_est2:BG679626
gb_est1:AL551470
st1:AW583133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: Aug 13, 2002 1:04 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est1:AW463601
gb_est1:AW383315
gb_est1:AI940071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1684.510000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query: US-10-040-803-7
Query length: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est2:BM389391
gb_est2:BG480197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est2:BE907706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTQ_spool/US10040803/runat_13082002_083351_7327/app_query.fasta_1.378
-Q-/cgn2_1/USPTQ_spool/US10040803/runat_13082002_083351_7327/app_query.fasta_1.378
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXY=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LICY=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=10 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-ALIGN=10 -MAXLEN=200000000 -USER-US104040803_eCGM1_1_2673
U-6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                          gb_est2:BI554641
gb_est2:BG967617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est2:BI413250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est1:AW383297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est2:BF180373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est1:AW462236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_htc:AK014645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score_list:
                                                                                gb_est2:BI334059
                                                                                                                                        gb_est2:BG892851
gb_est2:BG867549
                                                                                                                                                                                                                                   gb_est2:BI259237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est1:AL578261
                                                    gb_est1:AW202972
                                                                                                                                                                                                    gb_htc:AK005546
                                                                                                                                                                                                                                                                                           gb_htc:AK016509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of: US-10-040-803-7 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strd Orig
+ 1271.0
                                                                                                                                                                                                          490
490
487
483
480
478
473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 50
                                                                                                                                                                                                                                      . 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2SCORE
1992.87
1277.97
1260.82
1151.35
1109.97
1088.62
946.44
916.18
903.58
879.66
879.66
878.29
888.32
838.32
827.52
838.33
826.34
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
810.18
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               out_format : pfs
                                                                                7.6e-31
2.3e-30
2.5e-30
5.1e-30
                                                                                                                                                                                                                                                                                                                                                            8.2e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9e-40
                                                              5.0e-30
                                                                                                                                                                                                             4.0e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4e-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.4e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EScore
                                                                                                                                                                                                                                                                        2.1e-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4e-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e-102
                                                                                                                                                                                                                                                                                                                                                                                                                       ..6e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1e-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4e-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4e-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8e-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-48
   .9e-30
.8e-30
                                                                                                                                                                                                                                                                                                 .0e-32
                                                                                                                                                                                                                                                                                                                                                                                        .4e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1e-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4e-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0e-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1e-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   le-35
                                                                                                                                                                                                                                      , 2e-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIL md

ag962187 602826954F1 NFL006 PI

BI413250 602986390F1 NCI_CGAP_C

BI413250 602986390F1 NCI_CGAP_C

BI16860 602937954F1 NCI_CGAP_C

BF789214

NW30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK010640 Mus musculus ES cells AK004939 Mus musculus adult ma AK006271 Mus musculus adult ma AK006271 Mus musculus adult ma AL555870 AL55870 LTI_NEL006_PI AL578261 AL578261 LTI_NFL006_PI BG962187 602826954F1 NCI_CGAP_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Documentation
                            | AK016509 Mus musculus adult mat | BE590187 197182 BARC 5BOV Bos | BE1590187 7602970095F1 NIH, MGC_112 | AK005546 Mus musculus adult fe | BG892851 daa85d02-y1 Wellcome | BG87549 60278694F1 NCI_CGAP_1 | BI144893 602909736F1 NCI_CGAP_1 | BI144893 602909736F1 NIH_MGC_12 | BI34059 602997320F1 NIH_MGC_11 | BI334059 602997320F1 NIH_MGC_11 | BI34059 60299 | BI34059 6029 | BI34059 6029 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! AW463601 BP230013A20B9 SOARES I

AW383315 PML-HT0345-161199-002.

! AIJ440071 IL2-CT0031-290799-001.

! BM389391 UI-R-CNL-cjk-1-03-0-UI

! BG480197 602530380F1 NIH_MGC_.
                                                                                                                                                                                                                                                                                                                                                                                                                 | B1413250 602986390F1 NCI_CGAP_
| B1218460 602937954F1 NCI_CGAP_I
| B1763558 603050292F1 NIH_MGC_I1
| BF789214 602105109F1 NCI_CGAP_
| AW383305 PM1-HF0345-121199-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG679626
AL551470
AW583133
                                                                                                                                                                                                                                                                                                                          BG969117 602835094F1 NCI_CGAP_(
BI554641 603235988F1 NCI_CGAP_
BG967517 602833413F1 NCI_CGAP_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW462236 BP230008B20C12 Soares
BF180373 601804557F1 NCI_CGAP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE907706 601497734F1 NIH_MGC_7
BG824600 602728529F1 NIH_MGC_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW462598 BP230009B20E11 Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK014645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602627678F1 NCI_CGAP_S
AL551470 LTI_NFL006_PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iallc02.yl Human Pancı
         602826957F1 NCI_CGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus 10 days
                                                                       JOURNAL
```

```
gb_est2:BJ070867
gb_est2:BF047197
gb_est1:AU123750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est2:BF582351
gb_htc:BC008514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_htc:AK014645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBMED
                                                                                                         Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK014645 1323 bp mRNA linear HTC 19-JAN-200 Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4733401N09:BRAIN SPECIFIC SERINE PROTEASE-4 TYPE1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazzki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P. and Hayashizaki, Y. High-efficiency full-length CDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (strain:C57BL/6J) 10 days neonate skin cDNA to clone_lib:RIKEN_full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTC; CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK014645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murldae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone:4733401N09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK014645.1 GI:12852632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11042159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2049937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10349636
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FANTOM Consortium.
                                                            Direct Submission
                                                                                    Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451.50
451.50
448.50
445.00
442.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           685-690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            699.80
686.77
700.64
694.43
687.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.9e-30
5.2e-29
8.9e-30
2.0e-29
5.1e-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! BF582351 602101183F1 NCI_CGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I BC008514 Mus musculus, supp
BJ070867 BJ070867 NIBB Mochi
BF047197 dc04h08.y1 wellcome
BF047197 dc04h08.y1 wellcome
AU123750 AU123750 NT2RM2 Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTC 19-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes
```

Exploration Research Group, RIKEN Gemomic

Sciences Center (GSC),

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AK014645 from: 1 to: 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-040-803-7 x AK014645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
346 TGGGTGGTCACAGCCGCGCACTGCTTTAAGAGCAATATGGACAAACCATC 395
                                                                             296 TCCTCAAGAATGGCTCCCACCACTGTGCAGGCTCCCTGCTCACCAACCGC 345
                                                                                                                                                                                                                                                                                                                 146 TCTTAATCCTTCTGGTGCTTCTGACTTCCACAGCTCCCATCAGTGCTGCC 195
                                                                                                                                                                   246
                                                                                                                                                                                                                                                196
                       84 TrpVallleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTy 100
                                                                                                                           67
                                                                                                                                                                               50 1ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JRES
                                                                                                                                                                                                                                                                         34 ArgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVa 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                             96 ATGATGATCTCCAGACCTCCCCAGCACTCGGGTGGGGACCAGTTCAGCA 145
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetValValSerGlyAlaProProAlaLeu.GlyGlyGlyCysLeuGlyT 17
                                                                                                                                                                                                                                      ACCATCCGAGTGTCCCCAGACTGTGGGAAGCCTCAGCAGCTGAACCGGAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArg 83
                                                                                                                                                          TGTGGGAGGTGAGGACAGCATGGATGCCCAGTGGCCCTGGATTGTTAGCA 295
                                                                                                                                                                                                                                                                                                                                                           hrPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAla 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1271.00
Ratio: 4.605
milarity: 88.179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   data source:SPTR, source key:Q9ER10, evidence:ISS" 385 c 376 g 300 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="MGD:MGI:1903296"
/db_xref="taxon:10090"
/clone="4733401N09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="10 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="BRAIN SPECIFIC SERINE PROTEASE-4 TYPE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 75.399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313
```

```
COMMENT
                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block: 
LOCUS BE907706
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est2:BE907706
                                                                                                                                                                                                                                                                                    VERSION
                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              996 CAGTGGGGACACAGGAAGCTCCTAATCTAGGATCT 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 yGly.GlyAlaLeuArgAlaProSerGlnGlySer 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946 TGGGTGCAAAGGATCGTTCAAGGGGTGCACGTGCGCGGGTACTTGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 TrpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnG1 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      896 CGGAGCGCAACCGGCCCGGTGTGTACACCAGCCTCCTAGCTCACCGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 laGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  846 GGATGACCACTGGCTACTGACTGGCATAATCAGCTGGGGAGAGGACTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 GluargaspalaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GlnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 leHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIle 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 rIleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 TGGAAGGAGGGAACCCATGCAGACATTGCCCTGGTGCGCCTGGAACACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 TrpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 CATCCAGTTCTCTGAGCGGATCCTGCCCATCTGCCTACCTGACTCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 GGTCCCAGAAAGTAGGCATTGCTTGGGTGCTGCCTCACCCCAGGTATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 rgSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSer 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 TCTGTTCTCAGTATTGTTGGGGGCCTGGAAGCTGGGGAGCCCAGGCCCAA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 rLeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lAspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCAGGAAGCCATCACCGAGGGCATGCTGTGTGCTGGTTACCTGGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCGGGATGCTTGTCTGGGGGGGCTCCCCTGATGTGCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lyGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCATCATCGACTCCGAACTCTGCAAAAGCTTGTACTGGCGGGGAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGATGGAGTGCCCCTGCCCCACCCTCAGACCCTTCAGAAGCTGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCGTCTCCCCAAGACCGACTGCTGGATTGCCGGCTGGGGAAGCATC
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 470)
                                                                                                                                                                                                                                                                                                             mRNA sequence.
BE907706
                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                    BE907706.1 GI:10401537
                                                                                                                                                                                                                                                                                                                                                601497734F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899480
                                                                                                                                                                                                                                                                                                                                                                           470 bp
                                                                                       Mammalian Gene Collection (MGC
                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545
                                                                                                                                                                                                                                                                                                                                                                         EST 20-OCT-2000
```

cDNA Library Preparation: Life Technologies, Inc.

FEATURES

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-040-803-7 x BE907706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: BE907706 from: 1 to: 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                          418
                                                                                                                                                                                  368
                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                  101 LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
                                            151 Ile 151
                                                                                                                                      134
                                                                                                                                                                                                                                                                                                                                                                        268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                218
468 ATA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 ValGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 ATGGTGGTTTCTGGAGCGCCCCCAGCCCTGGGTGGGGGGCTGTCTCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 CTTCACCTCCCTGCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 rPheThrSerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA 34
                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyGlyCysLeuGlyTh 17
                                                                                                                   rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                        gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                           eGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgT 84
                                                                                          GGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCC
                                                                                                                                                                                  GTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCT 417
                                                                                                                                                                                                                                                                                                                                                                     GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
                                                                                                                                                                                                                                                                                                                                                                                              rpVallleThrAlaAlaH1sCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCAT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 468.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLAM9697 row: d column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:3899480"
/clone_lib="NIH_MGC_70"
/clone_lib="NIH_MGC_70"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage resistant)"
/note="Organ: pancreas; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            812.00
5.377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 t
```

```
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est2:BG824600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-10-040-803-7 x BG824600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: BG824600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                           105 CTTCACCTCCTGCTGCTGCTGCGCACAGCCATCCTCAATGCGGCCA 154
155 GGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCGGGTT
                                                                                                                                                                                                   17 rPheThrSerLeuLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA 34
                                                                                                                                                                                                                                                                      55
                                                                                                                                  34 rgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgVal 50
                                                                                                                                                                                                                                                                                                           1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh
                                                                                                                                                                                                                                                                 602728529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4868047 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG824600.1 GI:14172187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1737 row: i column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG824600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2: ECCRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected > 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Stratagene) and Superscript II RT (Life Technologies) 234 c 240 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     804.00
4.814
52.681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE: 4868047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 52.681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 22-MAY-2001
```

```
seq_documentation_block:
                                                                                                                   seq_name: gb_est1:AW462236
                   ACCESSION
                                                     DEFINITION
   VERSION
                                                                                                                                                                                                                                                                                     555 C 555
                                                                                                                                                                                        317 r 317
                                                                                                                                                                                                                      505 GGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCGCCGCCGCCCCCC
                                                                                                                                                                                                                                      301 GlyGlyAlaLeuArgAlaProSerGlnGlySerGlyAlaAlaAlaArgSe 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 yGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 LeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [51
                                                                                                                                                                                                                                                                                                                                                                                        67 aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyalaGl 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                      450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTTCTCTGTGCTGGGGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCG
                          AW462236 473 bp mRNA linear EST 24-FEB-20 BP230008B20C12 Soares normalized bovine placenta Bos taurus cDNA clone BP230008B20C12 5', mRNA sequence.
                   AW462236
AW462236.1 GI:7032404
                                                                                                                                                                                                                                                                                                                                                          .....TCCT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404
                                                                 EST 24-FEB-2000
                                                                                                                                                                                                                                                                                     alignment_block:
US-10-040-803-7 x AW462236
                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                     Align seg 1/1 to: AW462236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                               99
                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                     732.00
4.913
94.904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
```

```
KEYWORDS
116 SerArgSerGlnLysValGlyValAlaTrpValGluProHisProValTy 132
                                                                                             103 CAACCCAGTTCTCTGTGCTGCTGGGAGCCTGGCAGCTGGGGAACCCTGGC 152
                                                                                                                                                                                                                                                    82 rArgTrpVallleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysP 99
                                                                                                                                                                                                                                                                                                                                                                                    66 SerIleGlnLysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSe
                                                                                                                                                                                                                                                                                                                                                  roTyrLeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGly 115
                                                                                                                                                                                                                          CCGCTGGGTGCTCACGGCCGCCCACTGCTTCAAGGATAATCTGGACAAAC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 473 Std Error: 0.00
Plate: BP230008B20 row: C column:
Seq primer: AGCGGATAACAATTTCACACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@iuc.edu
Emoding for cattle EST sequencing was provided by the USDA National Funding for cattle EST sequencing was provided by the USDA National Funding for cattle EST sequencing was provided by the USDA National Funding for Cattle EST sequencing was provided by the USDA National Funding for University Genome Center PHRAP Suite.

Cross_match from Washington University Genome Center PHRAP suite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 473.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross_match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length. PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Lewin, H. A. W. M. K. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewin, H.A., Soares, M.B., Rebeiz, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: Not1; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="BP230008B20C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oaps: 0
Percent Identity: 82.166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pardinas, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gregory Dr., Urbana,
                                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu, L. and Larson
```

```
seq_name: gb_est2:BF180373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 CTCCTGGAAGGAGGGCTCCCGCGCTGACATCGCCCTGGTGCGCCTGGAGC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 AlaGlyGlnGlyProIleThr 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ysValProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGly 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerIleHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySe 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rSerTrpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGTCCCCATCATCGACTCAGCCACCTGCAGCCGCCTGTACTGGCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rIleGlnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCGTCCAGCTCTCCCGGACACCAACTGCTGGATTGCCGGCTGGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rgSerIleGlnPheSerGluArgValLeuProIleCysLeuProAspAla 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAGGTCCCAGGAGGTGGGTATCGCCTGGGCACAGCCCCACCCTGTGTA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCGGCCAGGCCCCATCACC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 935)
1 (bases 1 to 935)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF180373 933 1
601804557F1 NCI_CGAP_Mam5 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF180373
                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAM9309 row: a column: 16 High quality sequence stop: 732.
                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF180373.1 GI:11058515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
                       197
                       þ
                                                            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                   /strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:4035351"
/clone_lib="NCI_CGAP_Mam5"
                                                                                                                                                     /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                       279 c
                                                                                                                                                                                                                                                                                                                                                      on/Qualifiers
                       287 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    935 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus cDNA clone IMAGE:4035351 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 31-OCT-2000
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: BF180373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-040-803-7 x BF180373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 CCTCAAGAATGGCTCCCACCACTGTGCAGGCTCCCTGCTCACCAACCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 CTTAATCCTTCTGGTGCTGCTGACTTCCACAGCTCCCATCAGTGCTGCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                530 ATCCAGTTCTCTGAGCGGATCCTGCCCATCTGCTA.CCTGACTCCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 ATGATGATCTCCAGACCTCCCCCAGCACTGGGGGGACCAGTTCAGCAT 130
                                                                                                                                                                                     217 yGlnGlyProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG
                                                                                                                                                                                                                              674 CCA...TCCTCGACTCGAACTCTGGAAAAGCTGTAC...CGGGGGGAGCG 717
                                                                                                                                                                                                                                                                  201 ProIleIleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl 217
                                                                                                                                                                                                                                                                                                         627 AGGATGGGGTGCCCCGGCCC...ACCTCAGACCTTCAGAAGCTGAAGTGG 673
                                                                                                                                                                                                                                                                                                                                             184 lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200
                                                                                                                                                                                                                                                                                                                                                                                      579 CCGTCTCCCAAGACGAC.TGCTGGATTGGCGG.TGGGGAAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 rPheThrSerLeuLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetValValSerGlyAlaProProAlaLeuGlyGlyGlyCysLeuGlyTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTGGTCACAGCCGCGCACTGCTTTAAGAGCAATATGGACAAACCATCT 380
                                                                                                                                                                                                                                                                                                                                                                                                                        eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGGAGGGAACCCATGCAGACATTGCCCTGGTGCGCCTGGAACACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT
                                    AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGly..... 265
                                                                                                             luArgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250
                                                                            GAACGGAAGCCGTCTGGGGACCT.....GGGGTCCCGATGTGCCGGGTG
                                                                                                                                                   GTCAGGAGCCATCACGGGGCCT......GCTGGTGCTGGTACTGGAG
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710.50
3.230
70.968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 55.806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                              626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                             758
          834
```

94.631

```
alignment_scores:
                                                                                                                  ORIGIN
                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est1:AW463601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ON
RDS
                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AlaGinGlyGlyAlaLeuArgAlaPro 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGCGTGGGGGGAAAACATAAGAAACCCC 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACGCCGGGGACACCCTAACCCCGGGGAA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....CysAlaGluArgAsnArgProGlyValTyrIleSerLeuSerAlaH 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·····GAGCAGGGG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isArgSerTrpValGluLysIleValGlnGlyValGlnLeuArgGlyArg 297
                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: Ascovering 450. High quality sequence stop: 450. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 450 Std Error: 0.00 Plate: BP230013A20 row: B column: Seq primer: AGCGGATAACAATTTCACACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP230013A20B9 Soares normalized bovine placenta Bos taurus cDNA clone BP230013A20B9 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross_match from Washington University Genome Center PHRAP suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: ATTAACCCTCACTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences submitted are vector free and at least 200 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewinduiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Lewin, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW463601.1 GI:7033769
        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 450)
                                                                                                                                    73
                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                         /note-"Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: Not1; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
                        692.00
                                                                                                                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                        /sex="female"
                                                                                                                                                                                                                                                                                               /clone_lib="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                              /clone="BP230013A20B9"
                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
Length:
Gaps:
  149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION ACCESSION
                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.S.T
                                                                                                                                                                                       Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est1:AW383315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-040-803-7 x AW463601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 ysAlaGlyTyrLeuGluGlyGluArgAspAlaCysLeuGlyAspSer 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 CCTGTACTGGCGGGAGCCGGGCAGGGCGCCATCACCGAGGACATGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 ThrLeuGlnLysLeuLysValProIleIleAspSerGluValCysSerHi 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 CTGCCTGCCCGACTCCACCGTCCAGCTCTCTCCGGACACCAACTGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 eCysLeuProAspAlaSerIleHisLeuProProAsnThrHisCysTrpI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 LeuValArgLeuGluArgSerIleGlnPheSerGluArgValLeuProIl 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 AGCCCCACCCTGTGTACTCCTGGAAGGAGGGCTCCCGCGCTGACATCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 luProHisProValTyrSerTrpLysGluGlyAlaCysAlaAspIleAla 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 nLeuGlyAsnProGlySerArgSerGlnLysValGlyValAlaTrpValG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 AspAsnLeuAsnLysProTyrLeuPheSerValLeuLeuGlyAlaTrpG1 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 GCTGGGGAACCCTGGCCCAAGGTCCCAGGAGGTGGGTATCGCCTGGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GATAATCTGGACAAACCAACCCAGTTCTCTGTGCTGCTGGGAGCCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCTGGCTACCTGGAGGGGGAGCGCGACGCCTGTCTGGGCGATTCC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCTCCAGAAGCTGAAGGTCCCCATCATCGACTCAGCCACCTGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCCGGCTGGGGGAGCGTCCACGATGGAGTGCCCCTGTCCCACCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leSerGlyTrpGlySerIleGlnAspGlyValProLeuProHisProGln 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGTGCGCCTGGAGCGCCCATCCAGTTCTCTGAGCGCGTCCTGCCCAT
                                                                                                                                                                                                                                          Unpublished (A.J.G. Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Ludwig Institute for Prudente 109, 4 andar,
Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-HT0345-
161199-002-h07&t3=1999-11-1&&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                         HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                        Fax: +55-11-2707001
                                                                                                                                                                                                  Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW383315.1 GI:6887974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW383315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PM1-HT0345-161199-002-h07 HT0345 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW38331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 82.550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                     01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                     Sao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 04-FEB-2000
```

```
REFERENCE
                                                                                                                     VERSION
                                                                                                                                                            DEFINITION
                                                                                                                                                                                   seq_documentation_block:
LOCUS AI940071
                                                                                                                                                                                                                                          seq_name: gb_est1:AI940071
                                                                                                    KEYWORDS
                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AW383315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-040-803-7 x AW383315
                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                                                                 427
                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                              377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 sLeuProAspAlaSerIleHisLeuProProAsnThrHisCysTrpIles 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 uGlyAsnProGlySerArgSerGlnLysValGlyValAlaTrpValGluP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 GGGGAACCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGGGGC.TGGCAGCT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 AsnLeuAsnLysProTyrLeuPheSerValLeuLeuGlyAlaTrpGlnLe 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ment_scores:
                                                                                                                                                                                                                                                                                                                                                                               LeuGlnLysLeuLysValProIleIleAspSerGluValCysSerHisLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                             erGlyTrpGlySerIleGlnAspGlyValProLeuProHisProGlnThr
                                                                                                                                                                                                                                                                                 GTACTGGCGGGGATTGAACAGCGGACCC
                                                                                                                                                                                                                                                                                                                     uTyrTrpArgGlyAlaGlyGlnGlyPro 220
                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGCCCCCACCCTCAGACC
                                                                                                                                                                                                                                                                                                                                                          CTGCAGAAGCTGAAGGTTCCTATCATCGACTCGGAAGTCTGCAGCCATCT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTACCTGATGCCTCTATCCACCTCCCTCCAAACACCCCACTGCTGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValArgLeuGluArgSerIleGlnPheSerGluArgValLeuProIleCy 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCACCCTGTGTATTCCTGGAAAGAGGGTGCCTGTGCAGACATTGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCGTCTCGAGCGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roHisProValTyrSerTrpLysGluGlyAlaCysAlaAspIleAlaLeu 144
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 330)
                                                            Homo sapiens
                                                                                                      EST
                                                                                                                                       A194007
                                                                                                                                                          330 bp
IL2-CT0031-290799-001-A12 CT0031
                                                                                                                       AI940071.1 GI:5687052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 507.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-*Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657.00
5.256
99.206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="HT0345"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 97.619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                          Homo sapiens cDNA,
                                                                                                                                                                               mRNA
                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                                                                                                                                                                        426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
                                                                                                                                                        mRNA sequence
                                                                                                                                                                           EST 03-AUG-1999
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AI940071 from: 1 to: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-040-803-7 x AI940071/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                                                         103
                         153 PheSerGluArgValLeuProIleCys 161
                                                                                                                                                      136 luGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSerIleGln 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 GGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCATCCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 GAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGA
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 leThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProTyrLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 sAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerArgTrpVall 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 GlyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGlnLy
                                                                                                                                                                                                                                   nLysValGlyValAlaTrpValGluProHisProValTyrSerTrpLysG
                                                                                                 AAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAGCGCTCCATACAG
                                                                                                                                                                                                        GAAGGTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCTGGAAGG
                                                                                                                                                                                                                                                                                                               TCTGTGCTGCGGGGCCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCA
                                                                                                                                                                                                                                                                                                                                             SerValLeuLeuGlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGl 119
                                                                                                                                                                                                                                                                                                                                                                                                                     TCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project. This entry can be seen in the rully will condition (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-CT0031-290799-001-Al2&t3=1999-07-29&t4=1)
Seq primer: puc l8 forward
Seq primer: puc l8 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"organ: colon; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196./16 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 101 c 101 g 59 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CT0031"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                               130
                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
                                                                                                 30
                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
```

seq_name: gb_est2:BM389391

```
seq_documentation_block:
LOCUS BM389391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 bp mRNA linear EST 17-JAN-1
UI-R-CN1-cjk-i-03-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone
UI-R-CN1-cjk-i-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cervix library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-36, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Towa City, TA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM389391.1 GI:18189444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Norway rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer: M13 Forward
/lab_nost="DHIUB" (Life Technologies)
/note="Wector: pT773D-Pac (Pharmacia) with a modified
/note="Wector: pT73D-Pac (Pharmacia) with a dipose, normalized rat the prodiction of single-stranded circular DNA
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA template
/note="PT73D-Pac (PCR amplified inserts from a planid DNA t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="U1-R-CN1-cjk:1-03-0-UI"
/clone_1ib="U1-R-CN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear EST 17-JAN-2002
```

alignment_block:

Percent Similarity:

4.883 90.226 586.00

Gaps: 0
Percent Identity: 82.707

Length:

ORIGIN

BASE COUNT

168

178 g

155 t

alignment_scores:

Quality: Ratio:

```
and normalized libraries CSUS, CTUS, CNUS, CNUS and normalized libraies CSO, CTO, CTO, CWO, CWO, and CXO corresponding to plates R-CSOS-CBD through R-CSOS-CBO, R-CWOS-CCA, R-CWOS-CCB through R-CWOS-CCM, R-CWOS-CCM through R-CWOS-CCX, R-CWOS-CCB through R-CWOS-CCM, R-CWOS-CCM through R-CWOS-CCM, R-CWOS-CCM, R-CWOS-CCM through R-CWO-BWN, R-CWO-BWN through R-CWO-BWN, R-CWO-BWN,
                                                                                                                                                                                                                                                                                                            , bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI, bky-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI, bkz-a-011-0-UI, bkz-c-09-0-UI, bkz-d-100-UI, bkz-a-011-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI, blb-a-12-0-UI, bld-f-02-0-UI, blc-a-11-0-UI, blc-e-95-0-UI, bld-f-08-0-UI, bld-f-02-0-UI, bld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R-CA1-BLE. The resulting pool represented 20% of the final driver population. c) a pool of about 15,000 clones from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF, R-CA1-BKI, R-CA1-BKT, R-CA1-BLF, R-CA1-BLH through R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and R-CA1-BLE. The resulting pool represented 20% of
TAG_SEQ=GACCA"
201 c 1
                                                                                                                                       TAG_TISSUE=cervix
                                                                                                                                                                                         population.
TAG_LIB=UI-R-CN1
```

US-10-040-803-7 x BM389391/rev

ORIGIN

```
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BG480197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est2:BG480197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: BM389391 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 ProIleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyGluArgAs 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 GAGGATCGTGCAAGGGGTGCAGCTGCGAGGGCGCCTTGGCGGACAGTGGG 305
                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAspGlyA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGlyGlyGly 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCGGCCCGGCGTGTACACCAGCCTCCTAGCTCACCGCCCCTGGGTGCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpValGl 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGGCTACTGACGGCATAATCAGCTGGGGAGAGGGCTGCGCGGAGCGC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGluArg 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCATCACCGAGGACATGCTGTGTGCTGGTTACCTGGAAGGGAAGCGGGA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGACCCTGAACTCTGCAAAAGTTTGTACTGGCGGGGAGCTGGTCAGGAA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGly 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCTTGTCTGGGCGACTCTGGGGGGTCCCCTGATGTGCCAGGTGGATGACC
                                                                                                                                                                                                                        http://image.llnl.gov
Plate: LLCM1440 row: p column: 20
High quality sequence stop: 536.
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1001)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG480197
BG480197.1 GI:13412476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602530380F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4653955 5',
                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
/clone="IMAGE:4653955"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7;
                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1001 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
       Site_1: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 21-MAR-2001
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BG480197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-040-803-7 x BG480197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 CysTrpIleSerGlyTrp...GlySerIleGlnAspGly.ValProLeu. 189
                                                                                                                                                                                                                                                                                                                                                                                                             128 oHisProValTyrSerTrpLysGluGlyAlaCysAlaAsp...IleAlaL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 CCCATGGCTCTCGAGTCCCAAGAAGGTGGGTGTTGCCTGGGATGGAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 GCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCAGCAGCTGAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 ACCTTCACCTCCCTGCTGCTGGCTGGCTGGACAGCCATCCTCAATGCAG
                                                                                                                                                                                                                                                                                                                                  144 euValArgLeuGluArgSerIleGln.PheSerGlu.ArgValLeuProI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AAACATACCTGTTACTCTGTGCTGCTAGGGGGCCTGGCAAGCCTGGGGAA
653 CACCCAACCTACAGAGCCTGAAGAAAGCTAGAAAGGTTCCTAGTCATCGA
                      190 ..ProHisProGlnThrLeuGlnLysLeu...LysValPro.IleIleAs
                                                                                                                                                                                                                                      160 leCysLeuProAspAla.....SerIleHisLeuProProAsnThrHis 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 AlaArgIleProValProProAlaCysGlyLysProGlnGlnLeuAsnAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 ATGGTGGTTTCTGGAGCGCCACCCAGACCTGGGTGGGGGGCTGTCTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetValValSerGlyAlaProProAla.LeuGlyGlyGlyCysLeu.Gly
                                                                                            GAGTGGATCTCAGAGCTAGAGGGAGCCATCCAAGATGGAAGTAACCATTG
                                                                                                                                                                                         TCTGGCTAACTGATGCCTTCTATCCAACTCACACGTCACAAGAACGCAAT
                                                                                                                                                                                                                                                                                     GATGCAGTCTCGAGCGCTCCATACAAGTTCTCAGAGACGGGTACTGACCA
                                                                                                                                                                                                                                                                                                                                                                                       CCACCCTGTGTATTCCTGGACGGAAGGTGCCTGTGCAGACAATTGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nProGly...SerArgSerGlnLysValGlyValAlaTrp.ValGlu.Pr 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ysProTyrLeu.PheSerValLeuLeuGlyAlaTrp...GlnLeuGlyAs 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTGTGGGCGGCTGAGGACAGCACTGACAGCGAGTGGACCTGGATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gValValGlyGly.GluAspSerThrAspSerGluTrpProTrpIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrPheThrSerLeuLeuLeuAla.SerThrAlaIleLeuAsnAla. 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 255 c 292 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580.50
2.977
73.034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 64.045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                           602
                                                                                                                                                                                                                                                                                          552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102
                                                                                                 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202
```

6.3e-32

1.2e-31

2581

```
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-0b-916-366A-24 + 538.50 870.18 8.8e-41 11.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-016-366A-20 + 530.50 870.18 8.8e-41 11.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-016-366A-20 + 530.50 859.97 3.3e-40 11.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-016-366A-16 + 530.50 859.97 3.3e-40 11.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-016-366A-16 + 530.50 859.72 3.4e-40 11.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-016-366A-18 + 529.50 858.22 4.1e-40 11.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-016-366A-18 + 529.50 858.22 4.1e-40 11.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-078-404B-17 + 520.50 844.37 2.4e-39 103.
/cgn2_6/ptodata/J/ina/5B_COMB.seq:US-09-078-404B-17 + 520.50 844.37 2.4e-39 103.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-078-078-044B-17 + 514.50 833.89 9.3e-39 10.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-078-079-070A-4 + 511.50 833.89 9.3e-39 10.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-079-970A-4 + 511.50 833.89 9.3e-39 10.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-079-970A-1 + 508.00 822.81 3.8e-38 1709.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-088-651-1 + 508.00 822.81 3.8e-38 1709.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-088-651-6 + 467.50 748.78 3.0e-36 1109.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-088-651-6 + 467.50 744.42 8.9e-34 2413.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-088-651-6 + 467.50 741.63 13.3e-33 1077.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-088-651-6 + 467.50 741.63 13.3e-33 1079.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-088-651-6 + 467.50 741.63 13.3e-33 1079.
/cgn2_6/ptodata/J/ina/6B_COMB.seq:US-09-088-651-6 + 467.50 741.63 13.3e-33 249-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149-34 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            About: Results were produced by the GenCore software, version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: Aug 13, 2002 1:36 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM of: US-10-040-803-7 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query: US-10-040-803-7
Query length: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search time (sec): 48.690000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database sequences: 383533
Database length: 122816752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
                                          /cgn2_6/ptodata/1/ina/backfiles1.seq:5200340-5 + 452.00 724.93 1.1e-32 177.cgn2_6/ptodata/1/ina/backfiles1.seq:5200340-7 + 452.00 724.93 1.1e-32 267.cgn2_6/ptodata/1/ina/backfiles1.seq:5200340-7 + 452.00 720.02 2.0e-32 267.cgn2_6/ptodata/1/ina/5A_COMB.seq:US-09-643-603-1 + 452.00 719.71 2.1e-32 /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-643-219-12 + 451.00 719.14 2.3e-32 /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-812-087B-12 + 451.00 719.14 2.3e-32 /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-813-087B-12 + 451.00 719.14 2.3e-32 /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-851-350-12 + 451.00 719.14 2.3e-32 /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-132-154-12 + 451.00 719.14 2.3e-32 /cgn2_6/ptodata/1/ina/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-14 + /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-20 + /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-4 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -MODEL=frame+_P2n.model -DEV=x1h
-Q-/Cgn2_1/USPTO_Spool/US10040803/runat_13082002_083353_7361/app_query.fasta_1.378
-Q-/Cgn2_1/USPTO_Spool/US10040803/runat_13082002_083353_7361/app_query.fasta_1.378
-DB-ISSued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rn1
-GAPOP=12_000 -GAPEXI=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-COOPEXT=0.000 -GGAPOP=4.500 -GGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXI=0.500 -FGAPOP=6.000 -FGAPEXI=7.000 -YGAPOP=10.000
-YGAPEXI=0.500 -DELDOP=6.000 -DELEXIT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MING=10 -MALTEN=2000000000
-THR_SCORE=pct -THR_MAX=100 -THR_MING=10 -MODE=LOCAL
-TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-13 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strd Orig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EScore Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! Documentation
                     449.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        873.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1e-42
2.1e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2479
1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1077
```

```
seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-19 + 449.00 711.27 6.3e-
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-200-900A-1 + 443.50 706.32 1.2e-3
/cgn2_6/ptodata/1/ina/5B_COMB.seq:PCT-US94-00616-1 + 443.50 706.32 1.2e-3
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-027-337-1 + 438.50 695.81 4.5e-31
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-508-448C-15 + 434.50 697.30 3.8e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-016-366A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 14, Application US/09016366A Patent No. 5955431
                                                                                                                                                                                                                                Align seg 1/1 to: US-09-016-366A-14 from: 1 to: 1108
                                                                                                                                                                                                                                                                               US-10-040-803-7 x US-09-016-366A-14
                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stevens, Rich
APPLICANT: Huang, Chifu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1108 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: cDNA
53 lyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGln... 68
                                                 99 CCCTCGCCCAGCC.....AATCAGCGAGTGGGCATCGTGGGAG 136
                                                                                        37 lpro...proAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyG 53
                                                                                                                                          49 CTGCTGCTGCTGGGCACTGTCCCTCCTGGCTAGTCTGGTGTACTCAGC
                                                                                                                                                                                         21 LeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIleProVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wolf, Greenfield & Sacks, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΜA
                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                          68.100
                                                                                                                                                                                                                                                                                                                                                                             554.00
2.916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,637
ER: B0801/7093
                                                                                                                                                                                                                                                                                                                                   uaps: 9
Percent Identity: 41.577
                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                    98
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-20
                                                                                                                                                                                                                          Patent No. 5968782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                Sequence 20, Application US/08978404B
                                                                                                   APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINGGEN
NUMBER OF SEQUENCES: 74
                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                             813 GGTGACATACTTAGACTGGATCCACCGCTATGTC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 rLeuSerAlaHisArgSerTrpValGluLysIleVal 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 SerTrpGlyGluGlyCysAlaGluArgAsnArgProGlyValTyrIleSe 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 lyProLeuMetCysGlnValAspGlyAlaTrpLeuLeuAlaGlyIleIle 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669 TGCTGGA.....AATACCAGGAGAGACTCCTGCCAGGGCGATTCAGGGG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ySerIleGlnAspGlyValProLeuProHisProGlnThrLeuGlnLysL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 AlaSerIleHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGl 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 luArgSerIleGlnPheSerGluArgValLeuProIleCysLeuProAsp 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 lTyrSerTrpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 GlySerArgSerGlnLysValGlyValAlaTrpValGluProHisProVa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 AGCTCTTCCGGGTGCAGCTTCGTGAGCAGTATCTATACTATGGGGAC... 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 yrLeuPheSerValLeuLeuGlyAlaTrpGlnLeu.....GlyAsnPro 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 GTGGGTGCTCACTGCGGCACACTGTGTGGGACCGCACATCAAAAGCCCCAC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B72 CTATTACACGCCCGAGGGTGGG...GCAGACGTTGCCCTGCTGGAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: WOLL, CARREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 gTrpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTGGGGTGAGGGCTGCGCACAGCCCAACAAGCCTGGCATCTACACCCG 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyAlaGlyGlnGly......ProIleThrGluAsp...MetLeuCy 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sAlaGlyTyrLeuGluGlyGluArgAspAlaCysLeuGlyAspSerGlyG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euLysValProIleIleAspSerGluValCysSerHisLeuTyrTrpArg 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGACATTGATAATGACGAGCCTCTCCCACCTCCTTATCCTCTGAAGCAAG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCTCTACACGGGAGATGATTTTCCCATTGTCCATGATGGCATGCTGTG 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAGGTTCCCATTGTGGAAAACAGCCTGTGTGACCGGAAGTACCACACT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....CAGCTCCTCTTTGAACCGGATCGTGCTGCACCCCCA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTCCCTGTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCCT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \cdotsLys\mathtt{AsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerAr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-978-404B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-978-404B-20 from: 1 to: 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-040-803-7 x US-08-978-404B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/032,354
ETILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
372 CTATTACACGGCCGAGGGTGGG...GCAGACGTTGCCCTGCTGGAGCTTG
                                          131 lTyrSerTrpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuG 148
                                                                                          334 .....CAGCTCCTCTTTGAACCGGATCGTGCTGCACCCCCA 371
                                                                                                                                                                                       287 AGCTCTTCCGGGTGCAGCTTCGTGAGCAGTATCTATACTATGGGGGAC... 333
                                                                                                                                                                                                                                 100 yrLeuPheSerValLeuLeuGlyAlaTrpGlnLeu.....GlyAsnPro 114
                                                                                                                                         115 GlySerArgSerGlnLysValGlyValAlaTrpValGluProHisProVa 131
                                                                                                                                                                                                                                                                                                                                                                                   137 GACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGATTT 186
                                                                                                                                                                                                                                                                                                             83 gTrpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnLysProT 100 :||||||:::||||
                                                                                                                                                                                                                                                                                                                                                                                                            69 .....LysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerAr ::: ||| ||||||||||||||||||::: ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 lyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGln... 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 CCCTCGCCCAGCC.....AATCAGCGAGTGGGCATCGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 lPro...ProAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 CTGCTGCTGTGGGCACTGTCCCTCCTGGCTAGTCTGGTGTACTCAGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-NOV-9
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 LeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIleProVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-720-244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                      GTGGGTGCTCACTGCGGCACACTGTGTGGGACCGCACATCAAAAGCCCAC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554.00
2.916
68.100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/978,404B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 41.577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      в0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                83
```

```
seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08978404B Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 AGGTCCCTGTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCCCT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 luArgSerTleGlnPheSerGluArgValLeuProIleCysLeuProAsp 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ySerIleGlnAspGlyValProLeuProHisProGlnThrLeuGlnLysL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 GCCTCGGAGACCTTCCCCCCTGGGACATCGTGCTGGGTGACAGGCTGGGG 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 AlaSerIleHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGl 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MAST CELL PROTEASE TITLE OF INVENTION: FIBRINOGEN NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669 TGCTGGA.....AATACCAGGAGAGACTCCTGCCAGGGCGATTCAGGGG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 sAlaGlyTyrLeuGluGlyGluArgAspAlaCysLeuGlyAspSerGlyG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 euLysValProIleIleAspSerGluValCysSerHisLeuTyrTrpArg 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 813 GGTGACATACTACTTAGACTGGATCCACCGCTATGTC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 SerTrpGlyGluGlyCyshlaGluArgAsnArgProGlyValTyrIleSe 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 rLeuSerAlaHisArgSerTrpValGluLysIleVal 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 lyProLeuMetCysGlnValAspGlyAlaTrpLeuLeuAlaGlyIleIle 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            519
                 NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                  FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 02210-2211
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGACATTGATAATGACGAGCCTCTCCCACCTCCTTATCCTCTGAAGCAAG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAAGGTTCCCATTGTGGAAAACAGCCTGTGTGACCGGAAGTACCACACT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTGGGGTGAGGGCTGCGCACAGCCCAACAAGCCTGGCATCTACACCCG 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΜA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 Atlantic Avenue
617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stevens, Richard L.
VENTION: MAST CELL PROTEASE THAT CLEAVES
                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                60/032,354
                                                                                                                                                                                                                                                                                         US/08/978,404B
```

```
US-08-978-404B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-10-040-803-7 x US-08-978-404B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-978-404B-4 from: 1 to: 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1097 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 TGGGAGGACGAGAGGCTTCTGAAAGTAAGTGGCCCTGGCAGGTGAGCCTG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 AGATTTAAATTCAGCTTCTGGATGCATTTCTGTGGCGGCTCCCTCATTCA 216
                                                                                                                                                                                                                                          478 GACTTCTTGCTGGGTAACAGGCTGGGGGGACATTGATAGTGACGAGCCTC 527
                                                                                                                                                                                                                                                                                                                                       428 CATATCCACCCCATATCCCTGCCCCCTGGCTCGGAGACCTTCCCCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                  139 ysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSerGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 CCGGACCGTTGTGCACCCCCAC...TACTACACAGTCGAGGATGGG.... 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 yValAlaTrpValGluProHisProValTyrSerTrpLysGluGlyAlaC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 GlySerArgSerGln.....LysValG1 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 CCCACAGTGGGTGCTCACTGCGGCACACTGTGTGGGGACTGCACATCAAAA 266
                                                                                                                                                                                        189 euProHisProGlnThrLeuGlnLysLeuLysValProIleIleAspSer 205
                                                                                                                                                                                                                                                                      172 nThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyValProL 189
                                                                                                                                                                                                                                                                                                                                                                             156 ArgValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAs 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 GCCCAGAGCTCTTCCGTGTACAGCTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 GlnLysAsnGlyThr......HisHisCysAlaGlySerLeuLeuTh 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LeuLeuLeuAlaSerThr......AlaIleLeuAsnAlaAlaAr 34
                                                  578 AGCCTGTGTGATCGGAAGTACCACACTGGCCTCTACACAGGAGATGATGT 627
                                                                                          206 GluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGly...... 219
                                                                                                                                               528 TCCTGCCACCTTATCCTCTGAAGCAAGTGAAGGTCCCCATTGTGGAAAAC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 ysProTyrLeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnPro 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 rSerArgTrpVallleThrAlaAlaHisCysPheLysAspAsnLeuAsnL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 alGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIle 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 TTGCCCAGTCAAGCAGCGAGTGGGC.....ATTG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 gIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgValV 51
220 .ProIleThrGluAsp...MetLeuCysAlaGlyTyrLeuGluGlyGluA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.849
65.625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 10
Percent Identity: 40.625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
```

US-10-040-803-7 x US-09-016-366A-24

```
alignment_block:
                                                                                                  alignment_scores:
                                                                                                                                                             US-09-016-366A-24
                                    Percent Similarity:
                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1103 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Juence 24, Application US/09016366A Patent No. 5955431
                                                                                                                                                                              TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                           NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637 REFERENCE/DOCKET NUMBER: BONTELECOMMUNICATION INFORMATION: 517.720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/037,090
FILING DATE: 05-FEB-1997
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822 TTCACCGCTATGTC 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 alGluLysIleval 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  772 GGCCAATCGTCCTGGCATTTACACCCGGGTGACGTACTACCTGGACTGGA 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 uArgAsnArgProGlyValTyrTleSerLeuSerAlaHisArgSerTrpV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 722 GGTACCTGGCTGCAAGCAGGAGTGGTCAGCTGGGGTGAGGGCCTGCGCAGA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 GCGACTCCTGCCAGGGAGACTCAGGGGGCCCACTGGTCTGCAAAGTGAAG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 GlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGl 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        me: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-24
                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cumentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: January 30, 1998 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAsp 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 Atlantic Avenue
                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                 CDNA
                                      2.839
                                                                                                                                                                                                                       single
                                                                              536.50
                                  Percent Identity: 40.278
```

```
Align seg 1/1 to: US-09-016-366A-24
                                                                                                                                                                                      252 GlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGl 268
                                                                                                                                                                                                                                                               663 GCGACTCCTGCCAGGGAGACTCAGGGGGCCCACTGGTCTGCAAAGTGAAG 712
                                                                                                                                                                                                                                                                                              235 rgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAsp 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 AGCCTGTGTGATCGGAAGTACCACACTGGCCTCTACACAGGAGATGATGT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 euProHisProGlnThrLeuGlnLysLeuLysValProIleIleAspSer 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 .ProIleThrGluAsp...MetLeuCysAlaGlyTyrLeuGluGlyGluA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 GluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGly......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 TCCTGCCACCTTATCCTCTGAAGCAAGTGAAGGTCCCCATTGTGGAAAAC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 nThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyValProL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 ysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSerGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 GACTTCTTGCTGGGTAACAGGCTGGGGGGGACATTGATAGTGACGAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 CATATCCACCCCACATCCCTGCCCCCTGCCTCGGAGACCTTCCCCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 ArgValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAs 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 ..GCAGACATTGCCCTGCTGGAGCTTGAGAACCCTGTGAATGTCTCCACC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 GlySerArgSerGln......LysValGl 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 yValAlaTrpValGluProHisProValTyrSerTrpLysGluGlyAlaC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 GCCCAGAGCTCTTCCGTGTACAGCTT.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 CCCACAGTGGGTGCTCACTGCGGCACACTGTGTGGGACTGCACATCAAAA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 AGATTTAAATTCAGCTTCTGGATGCATTTCTGTGGCGGCTCCCTCATTCA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 TGGGAGGACGAGAGGCTTCTGAAAGTAAGTGGCCCTGGCAGGTGAGCCTG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 ysProTyrLeuPheSerValLeuLeuGlyAlaTrpGlnLeuGlyAsnPro 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 rSerArgTrpValIleThrAlaAlaHisCysPheLysAspAsnLeuAsnL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GlnLysAsnGlyThr......HisHisCysAlaGlySerLeuLeuTh 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 alGlyGlyGluAspSerThrAspSerGluTrpProTrpIleValSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 TTGCCCAGTCAAGCAGCGAGTGGGC.....ATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 gIleProValProProAlaCysGlyLysProGlnGlnLeuAsnArgValV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 CTGCTGCTGGCACTGTCCCCCCTGGCTAGTCTGGTGCACGCGGCCCC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LeuLeuLeuAlaSerThr.....AlaIleLeuAsnAlaAlaAr 34
GGCCAATCGTCCTGGCATTTACACCCGGGTGACGTACTACCTGGACTGGA 812
                                                              uArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpV 285
                                                                                                                               GGTACCTGGCTGCAAGCAGGAGTGGTCAGCTGGGGCGAGGGCTGCGCAGA 762
                                                                                                                                                                                                                                                                                                                                                                                           CCGGACCGTTGTGCACCCCCAC...TACTACACAGTCGAGGATGGG.... 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468
```

285 alGluLysIleVal 289

```
seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-008-271A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-09-008-271A-15
                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09008271A Patent No. 6203979
GENERAL INFORMATION:
                                                                                                                                                                     Align seg 1/1 to: US-09-008-271A-15 from: 1 to: 1081
                                                                                                                                                                                                                 US-10-040-803-7 \times US-09-008-271A-15
                                                                                                                                                                                                                                                                                Percent Similarity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813 TTCACCGCTATGTC 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 15:
                                                                                    43 GGCGCGCGGGGCGCTGCTGCTGCTGCTGCTGGCTCGGGCTGGACT 92
93 CAGGAAGCCGGAGTCGCAGGAGGCGGCGCCCTTATCAGGACCATGCGGCC 142
                                        29 eLeu.....AsnAlaAlaArgIleProValProProAlaCysGlyL 43
                                                                                                                               13 GlyCysLeuGlyThrPheThrSerLeuLeuLeuLeuAlaSerThrAlaIl 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: PROSTUT03
CLONE: 789927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: <Unknown> FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guegler, Karl J
Corley, Neil C.
                                                                                                                                                                                                                                                                                                       531.50
2.684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karl J.
                                                                                                                                                                                                                                                                                     Percent Identity:
                                                                                                                                                                                                                                                                                       36.039
```

```
seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 CGTTGGCCGTGGCAGGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 GACGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 rpLysGluGlyAlaCysAlaAspIleAlaLeuValArgLeuGluArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 T...TACTTCGTATCGAATATCTATCTGAGCCCTCGC....... 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 gSerGlnLysValGlyValAlaTrpValGluProHisProValTyrSerT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 CAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 Ala.....TrpGlnLeuGlyAsnProGlySerAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATGGTCCAGTTTGGC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 eHisLeuProProAsnThrHisCysTrpIleSerGlyTrpGlySerIleG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 IleGlnPheSerGluArgValLeuProIleCysLeuProAspAlaSerIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 yGlnGlyProileThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                628 GCCATCATAAACAACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 AAGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 lnAspGlyValProLeuProHisProGlnThrLeuGlnLysLeuLysVal 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 ys.....AspAsnLeuAsnLysProTyrLeuPheSerValLeuLeuGly 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 aGlySerLeuThrSerArgTrpValIleThrAlaAlaHisCysPheL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 GluTrpProTrpIleValSerIleGlnLysAsnGlyThrHisHisCysAl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 ysProGlnGlnLeuAsnArgValValGlyGlyGluAspSerThrAspSer 59 ::
                                                                                                                                                                                                                                                                                                                                                                                            778 AATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTGG 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 GGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTTGGCCTGTAACAAG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 luargAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnVal 250 :::|||||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   678 CCGCAAGGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCCAAGGCG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 ProllelleAspSerGluValCysSerHisLeuTyrTrpArgGlyAlaGl 217
                                                                                                                                                                                                                          284 rpValGluLysIleValGlnGlyValGlnLeuArgGlyArgAlaGlnGly 300
                                                                                                                                                                                                                                                                                  828 TCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGT 877
                                                                                                                                                                                                                                                                                                                                    267 aGluArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AspGlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAl 267
                                                                                                                                                                           878 GGATCCAGAAGCTGATG.....
                                                             904 GGCATGTCCCAGCCAGACCCCTCC 927
                                                                                                                301 GlyGlyAlaLeuArgAlaProSer 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAGGCCTCCACATT 527
```

seq_documentation_block:
; Sequence 20, Application US/09016366A

```
alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-016-366A-20
                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-016-366A-20 from: 1 to: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
149 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCA 198
                                                                                       99 GTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 148
                                                                                                                                                         53 lyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGlnLys 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Plumer, Elizabeth R.
REGISTION NUMBER: 36,637
REFERENTION NUMBER: BOINTELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION: 530
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
                                                                                                                                                                                                          49 CGCGGCCCCTGCCCAGGCCAGGCCTGCAGCGAGTGGGCATCGTTGGGG
                                                                                                                                                                                                                                36 oValProProAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyG 53
                                                                                                                                                                                                                                                                                                                                                                                          0-040-803-7 x US-09-016-366A-20
                                                                                                                                                                                                                                                                                                                                                                                                              ment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 600 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                           530.50
2.837
64.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 39.236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B0801/7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Gaps:
```

	MB D D D D D D D D D D D D D D D D D D D	
	TATE:	
	ADDRESSEE: V STREET: 600	
	APPLICANT: Stevens, R TITLE OF INVENTION: M TITLE OF INVENTION: F NUMBER OF SEQUENCES: CORPESSONIENCE	
	<pre>seq_documentation_block: Sequence 15, Application US/08978404B Fatent No. 5968782 GENERAL INFORMATION:</pre>	
٥.	seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-15	
	285 alGluLysIleVal 289 :::: 798 TCCACCACTATGTC 811	
285 797	268 uArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpV : ::::::::::::::::::::::::::::::::::	
268 747	252 GlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGl ::: :::::	
251 697	235 rgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAsp :::	
235 647	nrGluAspMetLeuCysAlaGlyTyrLeuGluGlyGluA ::: ::: 3TGACGACATGCTGTGTGCCGGGAACACCCGGA	
220 603	206 GluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGlyPro :::::: :::	
205 553	189 euProHisProGlnThrLeuGlnLysVeuLysValProIleIleAspSer	
189 503	172 nThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyValProL :	
172 453	156 ArgValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAs ::: :::	
155	139 ysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSerGlu 	
355	143 IALATTPVALGLUPTOHLSPTOValTyrSerTrpLysGluGlyAlac ::: ::	
12 30	GlyAlaTrpGlnLeuGlyAsnProG	
28	249 CCGCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTAC	
10	95AsnLeuAsnLysProTyrLeuPheSerValLeuLeu	

OPERATING SYSTEM:

```
alignment_block:
US-10-040-803-7 x US-08-978-404B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-978-404B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-978-404B-15 from: 1 to: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
156 ArgValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAs 172
                                                                                                                                                                                       123 lAlaTrpValGluProHisPro...ValTyrSerTrpLysGluGlyAlaC 139
                                                                                                                                                                                                                                                                                                                                     249 CCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTAC...... 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AsnGly.....ThrHisHisCysAlaGlySerLeuTeuThrSerAr 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 lyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGlnLys 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 CGCGGCCCCTGCCCAGGCCAGGCCCTGCAGCGAGTGGGCATCGTTGGGG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 oValProProAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 SerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIlePr 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AATCTGCTGCTGCCGCGCGCCCGTCCTG.....GCGAGCCGCGCCTA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                             CAGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGA.... 355
                                                                                                                                                                                                                                                                                   GlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLysValGlyVa 123
                                                                                                                                                                                                                                                                                                                                                                            .....AsnLeuAsnLysProTyrLeuPheSerValLeuLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gTrpValIleThrAlaAlaHisCys.....PheLysAsp.... 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530.50
2.837
64.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOS
for Windows Version
                                                                                                                                                                                                                                         .....TACCAGGACCAGCTGCTGCCGGT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/978,404B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.236
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 16, Application US/09016366A
Patent No. 5955431
                                                                                                           FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 euProHisProGlnThrLeuGlnLysLeuLysValProIleIleAspSer 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 nThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyValProL 189
                                             REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELLEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               748 GCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 uArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 GlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGl 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 rgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAsp 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 ......IleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyGluA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               554 CACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 GATGCCGTGCTGGGTCACTGGCTGGGCGATGTGGACAATGATGAGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 CACGTCCACACGGTCACCCTGCCCCTGCCTCAGAGACCTTCCCCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       798 TCCACCACTATGTC 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 alGluLysIleVal 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604 CCGCATCGTCCGTGACGACATGCTGTGCCGGG.....AACACCCGGA 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 GluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGlyPro..... 220
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
TELEX:
                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 Atlantic Avenue
                          617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                   US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453
```

16:

```
alignment_block: US-10-040-803-7 \times US-09-016-366A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-016-366A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                      523
                                                                                                                                                                                                                           473
                                               573
                                                                                                                                                                               189
                                                                                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                                  423
                                                                                                                                                                                                                                                                                                                                                                                                        375
                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 GlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLysValGlyVa 123
      221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 lAlaTrpValGluProHisPro...ValTyrSerTrpLysGluGlyAlaC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 GTGGGTGCTGACCGCGGCGCACTGCCTGGGACCGGACGTCAAGGATCTGG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 CGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 SerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIlePr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 AGCCTGCTGCTGCCGCCCTGCCCGTCCTG.....GCGAGCCGCGCCTA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 lyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGln... 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 CGCGGCCCCTGCCCCAGTCCAGGCCCTGCAGCAAGCGGGTATCGTCGGGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 oValProProAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                             GluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGlyPro....
                                                                                                                                                                                                                    GATGCCGTGCTGGGTCACTGGCTGGGCGATGTGGACAATGATGAGCCCC
                                                                                                                                                                                                                                                      nThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyValProL 189
                                                                                                                                                                                                                                                                                                             CGCGTCCACACGGTCATGCTGCCCCCTGCCTCGGAGACCTTCCCCCCGGG
                                             CACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGT 622
                                                                                                                                  TCCCACCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAAC
                                                                                                                                                                                                                                                                                                                                                        ArgValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAs 172
                                                                                                                                                                                                                                                                                                                                                                                                    ysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSerGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCAGGATCATCGTGCACCCACAGTTCTACATCATCCAGACTGGA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTAC...... 305
                                                                                                                                                                           euProHisProGlnThrLeuGlnLysLeuLysValProIleIleAspSer 205
.....IleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyGluA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gTrpValIleThrAlaAlaHisCysPhe.....LysAsp....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....LysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerAr 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....AsnLeuAsnLysProTyrLeuPheSerValLeuLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1154 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530.50
2.837
64.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....TACCAGGACCAGCTGCTGCCAGT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.583
                                                                                                                                    572
                                                                                                                                                                                                                        522
                                                                                                                                                                                                                                                                                                               472
                                                                                                                                                                                                                                                                                                                                                                                                    422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
```

```
alignment_block:
                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                            US-08-978-404B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-404B-11
US-10-040-803-7 x US-08-978-404B-11
                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08978404B Patent No. 5968782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,63
REFERENCE/DOCKET NUMBER: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 GlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGl 268
|||:::|||||| ||||||::::::|||||| |||||||:::
717 GGCACCTGGCTACAGGCGGGGCGTGGTCAGCTGGGACGACGACGGCTGTGCCCA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 uArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 rgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAsp 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    623 CCGCATCATCCGTGACGACATGCTGTGTGCCGGG.....AACAGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              817 TCCACCACTATGTC 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                767 GCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGA 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 GGGACTCCTGCAAGGGCGACTCTGGAGGGCCCCCTGGTGTGCAAGGTGAAT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 alGluLysIleVal 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 600 A CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version NATA:
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-720-35
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                        nucleic acid
                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 Atlantic Avenue
                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolf,
                                                           530.50
2.837
64.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenfield & Sacks, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60/032,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/978,404B
                                                                                                                                                                                                                                                                                                                                                                                                                                              36,637
                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                 в0801/7090
                                                                                                        Length:
                                                                                  Gaps:
                                                              39.583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666
```

```
Align seg 1/1
                                                                                                                                                                                                                            717
817 TCCACCACTATGTC 830
                                                   285 alGluLysIleVal 289
                                                                                                                                            268 uArgAsnArgProGlyValTyrIleSerLeuSerAlaHisArgSerTrpV 285
                                                                                                                                                                                                                                                              252 GlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGl 268
                                                                                                                                                                                                                                                                                                                                   667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573 CACATTIGIGACGCAAAATACCACCTIGGCGCCTACACGGGAGACGACGI 622
                                                                                                                                                                                                                                                                                                                                                                                                                                    623 CCGCATCATCCGTGACGACATGCTGTGCCGGG.....AACAGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 GluValCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGlyPro....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 GATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 lAlaTrpValGluProHisPro...ValTyrSerTrpLysGluGlyAlaC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 GlyAlaTrpGlnLeuGlyAsnProGlySerArgSerGlnLysValGlyVa 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 euProHisProGlnThrLeuGlnLysLeuLysValProIleIleAspSer 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 ysAlaAspIleAlaLeuValArgLeuGluArgSerIleGlnPheSerGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 CGCGACCGATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 GTGGGTGCTGACCGCGCGCACTGCCTGGGACCGGACGTCAAGGATCTGG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 GTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 lyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGln... 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 .....LysAsnGlyThrHisHisCysAlaGlySerLeuLeuThrSerAr 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 CGCGGCCCCTGCCCAGTCCAGGCCCTGCAGCAAGCGGGTATCGTCGGGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 oValProProAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 AGCCTGCTGCTGGCGCGCTGCCGTCCTG.....GCGAGCCGCGCCTA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SerLeuLeuLeuAlaSerThrAlaIleLeuAsnAlaAlaArgIlePr 36
                                                                                                                                                                                                                                                                                                                           GGACTCCTGCAAGGGCGACTCTGGAGGGCCCCTGGTGTGCAAGGTGAAT 716
                                                                                                                                                                                                                                                                                                                                                          rgAspAlaCysLeuGlyAspSerGlyGlyProLeuMetCysGlnValAsp 251
                                                                                                       GCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGA 816
                                                                                                                                                                                                              GGCACCTGGCTACAGGCGGGCGTGGTCAGCTGGGACGAGGGCCTGTGCCCA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nThrHisCysTrpIleSerGlyTrpGlySerIleGlnAspGlyValProL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCAGGATCATCGTGCACCCACAGTTCTACATCATCCAGACTGGA.... 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgValLeuProIleCysLeuProAspAlaSerIleHisLeuProProAs 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCCACCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAAC 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCGTCCACACGGTCATGCTGCCCCCTGCCTCGGAGACCTTCCCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....IleThrGluAspMetLeuCysAlaGlyTyrLeuGluGlyGluA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....TACCAGGACCAGCTGCTGCCAGT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....AsnLeuAsnLysProTyrLeuPheSerValLeuLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: US-08-978-404B-11 from: 1 to: 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472
```

```
alignment_block: US-10-040-803-7 \times US-09-016-366A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-016-366A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
; Sequence 18, Application US/09016366A
; Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-016-366A-18
                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-016-366A-18 from: 1 to: 1137
                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/037,09
ETILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
60/037,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wolf, Greenfield &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stevens, Richard L. APPLICANT: Huang, Chifu
70 AsnGly......ThrHisHisCysAlaGlySerLeuLeuThrSerAr 83
                                        97 GTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 146
                                                                          53 lyGluAspSerThrAspSerGluTrpProTrpIleValSerIleGlnLys 69
                                                                                                                     47 CGCGGCCCTGCCCCAGGCCAGGCCCTGCAGCGAGTGGGCATCGTCGGGG
                                                                                                                                                       36 oValProProAlaCysGlyLysProGlnGlnLeuAsnArgValValGlyG
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                              3 AATCTGCTGCTGCGCGCTGCCCGTCCTG.....GCGAGCCGCGCCTA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 600 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                January 30,
N: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                        529.50
2.832
64.931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 39.236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B0801/7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sacks,
                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                         53
                                                                                                                     96
```

147	CACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCCCA 196
83	gTrpVallleThrAlaAlaHisCysPheLysAsp 94
197	## CTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGG 246
95	
247	CCGCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTAC
107	G
285	
123	
308	CAGCAGGATCATCGTGCACCACAGTTCTACACCGCCCAGATCGGA 353
139	¥
54	GCGGACATCGCCCTGCTGGAGCTGGAGGAGCCGGTGAACGTCTCCAGC 401
156	
402	::: CACGTCCACACGGTCACCCTGCCCCCTGCGTCAGAGACCTTCCCCCCGGG 451
172	
452	eargccgrgcrgggrcacrggcrggggcgargrggacaargargagcgcc 501
189	
502	TCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAAC 551
206	GluvalCysSerHisLeuTyrTrpArgGlyAlaGlyGlnGlyPro 220
552	
221	
602	ccccarccrcarcaccacarccrcrcrccccccc
235	
646	GGGACTCATGCCAGGCGACTCCGGAGGGCCCCTGGTGTGCAAGGTGAAT 695
252	GlyAlaTrpLeuLeuAlaGlyIleIleSerTrpGlyGluGlyCysAlaGl 268
696	
268	
746	
285	5 alGluLysIleVal 289
706	

•

```
OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hed:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_032802:*

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1981.DAT:*

3: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1982.DAT:*

4: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1983.DAT:*

5: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1984.DAT:*

6: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1985.DAT:*

7: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1986.DAT:*

8: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1987.DAT:*

9: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA1987.DAT:*
                    10:
11:
12:
13:
14:
15:
15:
16:
17:
18:
19:
20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              August 13, 2002, 08:43:12; Search time 30.51 Seconds (without alignments) 1154.061 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-040-803-7
1720
1 MVVSGAPPALGGGCLGTFTS.....AQGGGALRAPSQGSGAAARS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \begin{array}{c} \text{GenCore version 4.5} \\ \text{Copyright (c) 1993 - 2000 Compugen Ltd.} \end{array}
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA198B.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA198B.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA198B.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA199B.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
(SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10 1/14	10 171	9 172	8 172	7 172	6 172	5 172	4 172	3 172	2 172	1 172	Result No. Score	
4 99.7											Query	æ
322	3	351	325	325	317	317	317	317	317	317	Length DB	
22	ر د	22	22	22	22	22	21	21	20	20	:	
AAU17038	AAII23751	AAU16966	AAU17037	AAU23215	AAB80259	AAY72890	AAY93689	AAB11700	AAY13391	AAY06482	ID	
novel	Novel human enzyme	Human novel secret	Human novel secret	Novel human enzyme	Human PRO343 proce	Human serine proce	Amino acid sequenc	Human serine proce	Amino acid sequenc	Human tumour-assoc	Description	

ALIGNMENTS

XX PR PR PR PR	PD XX	FF FF F X C	XX XX DE XX DT XX	RESULT AAY064 ID A XX AC A
		Key Peptide Protein Protein	EP-1999 (fintumour-asson tumour-asson tumour	RESULT 1 AAYO6482 ID AAYO6482 standard; XX AC AAYO6482;
98US-0109304. 98US-0070440. 98US-0083500. 98US-0086414. 98US-0088742. 98US-0107783.	/note= "N-glycosylated" 99WO-US00106.	Location/Qualifiers 132 "signal peptide" /note- "signal peptide" 33317 /note- "mature protein" 70	ry) protein PRO343. tumour; diagnosis;	3; Protein; 317 AA.
			therapy;	
			human	

```
Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
       Secreted protein; transmembrane protein; human; enterocolitis; zollinger-Ellison syndrome; gastrointestinal ulceration;
                                            Amino acid sequence of protein PRO343.
                                                                     25-JUN-1999 (first entry)
                                                                                                                       AAY13391 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents human PRO343 (UNQ302), a protein encoded by the novel cDNA clone DNA43318 (see AAX87259). Amplification of DNA43318 was observed in primary lung tumours and in primary colon tumours, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed to PRO343 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may be useful targets for the diagnosis act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer diagnoseric wite
                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic
                                                                                                                                                                                                           301
                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                        Antibody against proteins expressed tumor diagnosis and treatment
                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Botstein
                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                                               _
                                                                                                                                                                                              GGALRAPSQGSGAAARS 317
                                                                                                                                                                                                                                                 DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                         GSIQDGYPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG
                                                                                                                                                                                                                                                                       gsiqdgvplphpqtlqklkvpiidsevcshlywrgagqgpitedmlcagylegerdaclg
                                                                                                                                                                                                                                                                                                                                                                                                                   MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE 60
                                                                                                                                                                                 ggalrapsqgsgaaars 317
                                                                                                                                                                                                                                                                                                                                                                                  WPWIVSIOKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK 120
                                                                                                                                                                                                                                                                                                                                                                       wpwivsiqkngthhcagslltsrwvitaahcfkdnlnkpylfsvllgawqlgnpgsrsqk 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity
317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Fig 12; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A,
                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1720; DB 20; 100.0%; Pred. No. 3.2e-147; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney AL,
                                                                                                                      317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in neoplastic cells, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
      WPI; 199
N-PSDB;
                                                                                                                                                                                                                                 29-OCT-1997;
31-OCT-1997;
31-OCT-1997;
31-OCT-1997;
03-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                       24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
24-OCT-1997;
27-OCT-1997;
27-OCT-1997;
28-OCT-1997;
New isolated human genes and polypeptides used
                                                                                                                                                                                                                                                                                                                    29-0CT-1
29-0CT-1
29-0CT-1
                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                            12-NOV-1997;
                                                                                                                                                                                                                                                                                              29-OCT-1997;
29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L7-SEP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09914328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-thrombotic; wound healing; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7-SEP-1997
                           1999-229533/19.
DB; AAX52262.
                                                           Goddard A,
                                                                                                                       97US-0066466.
97US-0066770.
97US-0066511.
                                                                                                                                                                                          97US-0063870.
97US-0064248.
97US-0064248.
97US-0065186.
97US-0065846.
97US-006593.
                                                                                                                                                                                                                                                                                                                 9705-0063541
9705-0063542
9705-0063544
9705-0063549
9705-0063564
9705-0063564
9705-0063704
9705-0063703
9705-0063733
9705-0063733
                                                                                                             97US-0066453
                                                                                                                                                                      97US-0066120
97US-0066364
                                                                                                                                                                                                                                                                                  97US-
97US-
97US-
97US-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0059122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US19330
                                                           Gurney
                                                            Æ,
                                                            Pennica
```

SSSSSSSS

B δÃ 밁 δÃ

Ď

WI,

in,

e.g.

treatment of

밁 δÃ B δÃ 밁 Qy

```
RESULT
AAB11700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            688xx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Б
OS XWW XEX DXX
                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with abnormal keratinocyte differentiation (e.g. poriasis, epitheliai cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as Alzheimer fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tunor drugs. PRO533 may be used in the treatment bf Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO279 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. entercoolitis, Zollinger-Ellison syndrome, gastrointestinal clean congenital microvillus atrophy), skin diseases associated ulceration and congenital microvillus atrophy), skin diseases associated ulceration and congenital microvillus atrophy), skin diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY13344-403 represent secreted and transmembrane human proteins
The cDNA sequences are obtained from cDNA libraries, prepared from the cDNA libraries of the control of the cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 98; 320pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                BSSP4; serine protease; human; hBSSP4; mouse; mBSSP4; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
Homo sapiens
                                                                                                                                      Human serine protease BSSP4 (hBSSP4) SEQ ID NO:2.
                                                                                                                                                                                     23-OCT-2000
                                                                                                                                                                                                                                                                                 AAB11700 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VGVAMVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 WPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity tes 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | mvvsgappalgggclgtftsllllastailnaaripvppacgkpqqlnrvvggedstdse 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE 60
                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG
                                                                                                                                                                                                                                                                                                                                                                                                 ggalrapsqgsgaaars 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGALRAPSQGSGAAARS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt gsiqdgvplphpqtlqklkvpiidsevcshlywrgagqgpitedmlcagylegerdaclg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vgvawvephpvyswkegacadialvrlersiqfservlpiclpdasihlppnthcwisgw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1720; DB 20; ilarity 100.0%; Pred. No. 3.2e-147; Conservative 0; Mismatches 0;
                                                                                                                                                                                     (first entry)
                                               inflammation; prostate; testis; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO264 can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
밁
                                                                  δÃ
                                                                                                        밁
                                                                                                                                        Ş
                                                                                                                                                                              밁
                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        initially isolated in a human brain CDNA library using degenerate PCR primers (AAA61714-A61715) based on conserved regions of serine proteases. The BSSP4 serine proteases and nucleotides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland and testis) as diagnostic markers for diseases associated with altered BSSP4 expression levels. Such diseases include Alzheimer's disease, oedema (dropsy), cancer or inflammation of brain, prostate, testis or bone. Sequences AAA61695-A61703 ans AAA61793 represent cDNAs encoding human BSSP4 variants (hBSSP4), and sequence AAA61704 represents cDNA encoding murine BSSP4 (mBSSP4). Sequences AAB11700 -B11708 represent human BSSP4 murine BSSP4 (mBSSP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising BSSP4 nucleic acids; transgenic animals in which the expression level of BSSP4 can be varied; and an mBSSP4 knockout mouse. The invention additionally encompasses anti-BSSP4 antibodies and methods of production of such antibodies, methods of BSSP4 detection using the antibodies, and the use of BSSP4 proteins or fragments as diagnostic markers for certain medical conditions. Nucleotides encoding BSSP4 were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel serine proteases designated BSSP4 (AABI1700-B11709), and to nucleic acids encoding them (AAA61695-A61704, AAA61799). The invention also relates to vectors and transformants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200031277-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease BSSP4 and antibodies recognizing BSSP4 for assay and diagnosis of diseases in which BSSP4 expression is altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 66-67; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FUSO ) FUSO PHARM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variants (hBSSP4), and sequence AAB11709 represents murine BSSP4
                                    241
                                                                      241
                                                                                                          181
                                                                                                                                            181
                                                                                                                                                                              121
                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                     2000-400084/34.
                                                                                                    VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW 180
                                                                                                                                                                                                                                                 wpwivsigkngthhcagslltsrwvitaahcfkdnlnkpylfsvllgawqlgnpgsrsqk 120
                                                                                                                                                                                                                                                                      WPWIVSIQKNGTHHCAGSLLISRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK 120
GGALRAPSQGSGAAARS 317
                                                   DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                              vgvawvephpvyswkegacadialvrlersiqfservlpiclpdasihlppnthcwisgw
                                  dsggplmcqvdgawllagiiswgegcaernrpgvyislsahrswvekivqgvqlrgraqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okui A, Kominami K, Yamaguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0347813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-JP06472
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1720; DB 21; Length 317; 100.0%; Pred. No. 3.2e-147;
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitsui
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                         300
                                                                                                              240
                                                                                                                                                240
                                                                                                                                                                                    180
```

0;

δÃ

Db

301 301

317

```
AAY93689
                                                                               22-DEC-1998;
08-MAR-1999;
02-JUN-1999;
01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
                          Botstein Wood WI;
WPI; 2000-452188/39.
N-PSDB; AAA46914.
                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                  Region
                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                 16-DEC-1999;
                                                                                                                                                                                   29-JUN-2000
                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                   WO200037640-A2
                                                                                                                                                                                                                                                                                                     Active-site
                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumourigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of novel polypeptide PRO343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY93689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93689 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ≀egion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                  D,
                                    Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                98US-0113296.
99WO-US05028.
99WO-US12252.
99WO-US20111.
99WO-US21090.
99WO-US28313.
                                                                       99WO-US28565
                                                                                99WO-US28409
99WO-US28301
                                                                                                                                                                99WO-US30095
                                                                                                                                                                                                                                              /note= "0
273..279
                                                                                                                                                                                                                             /note=
310..31
                                                                                                                                                                                                                                                                 /note= "|
178..182
                                                                                                                                                                                                                                                                                                     /note-
86..92
                                                                                                                                                                                                                                                                                                                                       70..74
/note=
71..77
                                                                                                                                                                                                                                                                                                                                                                           /note=
52..58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; neoplastic cell growth; cell proliferation
                                                                                                                                                                                                                                                                                                                      /note=
77..83
                                                                                                                                                                                                                                                                                                                                                                                            /note=
16..22
                                                                                                                                                                                                                                                                                                                                                                                                              /note=
13..19
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-myristoylation site" 12..18
                                                                                                                                                                                                                                                                                            'note-
                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                  Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                         "active site for serine protease"
                                                                                                                                                                                                                                                                                                           "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                   "N-myristoylation site"
                                                                                                                                                                                                                                     "N-myristoylation site"
                                                                                                                                                                                                                                                        "glycosylation attachment
                                                                                                                                                                                                                                                                        "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                             "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "prokaryotic membrane lipoprotein attachment site"
                                  Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                  Hillan
                                  ζ,
                                  Lawrence DA,
                                                                                                                                                                                                                                                        site"
                                  Roy
                                  MA
```

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                           AAY72890
                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                              Human; serine protease; protease C-E; therapy; desquamation; skin care; laundry detergent; shampoo; cleaning agent; hair care; skin flaking; neurodegenerative disorder; dermatological; immunogenic; proteolytic.
                         14-AUG-2000; 2000WO-US22117.
                                                     08-MAR-2001.
                                                                                                           Homo sapiens.
                                                                                                                                                                                                           Human serine
                                                                                                                                                                                                                                                                                          AAY72890 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO349, PRO357, PRO715, PRO117, PRO509, PRO833 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and resident in the treatment and diagnosis of neoplastic cell growth
                                                                                 WO200116288-A2
                                                                                                                                       chromosome 16p13.3.
                                                                                                                                                                                                                                       31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and proliferation in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New anti-polypeptide antibody useful in the treatment and neoplastic cell growth and proliferation -
                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                            301 GGALRAPSQGSGAAARS
                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE
                                                                                                                                                                                                                                                                                                                        ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                  DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggalrapsqgsgaaars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGVAMVEPHPYYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mvvsgappalgggclgtftsllllastailnaaripvppacgkpqqlnrvvggedstdse 60
                                                                                                                                                                                                                                                                                                                                                                                                                     dsggplmcqvdgawllagiiswgegcaernrpgvyislsahrswvekivqgvqlrgraqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vgvawvephpvyswkegacadialvrlersiqfservlpiclpdasihlppnthcwisgw 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 12; 220pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                         protease, protease C-E.
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                 317
                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1720; DB 21;
Pred. No. 3.2e-147;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
```

0

31-AUG-1999;

```
XXX XXX XXX XXX
                                                                                                                                                                                                                                                                                                                                                                 Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA XXX PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
          Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
                                                                                                                                                                   Human PRO343 protein.
                                                                                                                                                                                                                                  24-APR-2001
                                                                                                                                                                                                                                                                                                                                                       AAB80259 standard; Protein; 317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate, small intestine, stomach, spleen, fibroblasts, epidermis, cerebellum, cerebral cortex, pituitary and hippocampus. Protease C-E is useful for treating an imbalance of desquamation, by topical application. A non-pharmaceutical composition comprising the protein may be formulated as a laundry detergent, shampoo, hard surface cleaning composition, dish care cleaning composition, skin care composition and hair care composition. Protease C-E is useful for treating and preventing skin flaking, neurodegenerative disorders and dermatological pathologies. It is less immunogenic to sensitive individuals and it provides efficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteolytic activity in a non-natural environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a human serine protease, protease C-E which is a member of the S1 serine protease family. Protease C-E gene is located on chromosome 16p13.3 and is expressed in pancreas, placent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 1; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGVAMVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggalrapsqgsgaaars 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGALRAPSQGSGAAARS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \tt dsggplmcqvdgawllagiiswgegcaernrpgvyislsahrswvekivqgvqlrgraqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gsiqdgvplphpqtlqklkvpiidsevcshlywrgagqgpitedmlcagylegerdaclg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-226681/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 AA;
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
antiinfertility; antidiabetic; antiviral; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrade-Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1720; DB 22; Length 317; Pred. No. 3.2e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
```

Qy

121 VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW 180

ρy

61

61

```
밁
                                                                                  Query Match
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Filvaroff E, rung
Godowski PJ, Grima
Godowski PJ, Pan J,
                                                                                                                                        The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                             Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease)
                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 98; 393pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF72420
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-081051/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
Filvaroff E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200104311-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L6-DEC-1999;
Local Similarity
                                                                                                                         317 AA;
                                                        100.0%; ilarity 100.0%; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fong S, Gao W, Gerber I
Grimaldi CJ, Gurney AL,
an J, Paoni NF, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US04414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US30999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US28313.
99WO-US30095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US28214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US23089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US21090.
99WO-US21547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0145698
99US-0146222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US20594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0143048
                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desnoyers L,
W, Gerber H,
                                                                  Score 1720; DB 22;
Pred. No. 3.2e-147;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillan KJ,
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eaton DL,
                                                        0,
                                                       Indels
                                                                              Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ME, God
Kljavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard A;
                                                     0;
                                                    Gaps
    60
                                                     0;
```

```
RESULT
AAU23215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                            밁
  24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU23215 standard; Protein; 325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200155301-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human enzyme polypeptide #301.
                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU23215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                           -MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggalrapsqgsgaaars 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGALRAPSQGSGAAARS 317
  2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-0184664.
2000US-0184664.
2000US-019874.
2000US-0199874.
2000US-02198123.
2000US-0214886.
2000US-0214887.
2000US-0214887.
2000US-0214887.
2000US-0214887.
2000US-0214887.
2000US-0214987.
2000US-0214987.
2000US-0214987.
2000US-0214987.
2000US-0224518.
2000US-0224518.
2000US-02252514.
2000US-0225257.
2000US-0225266.
2000US-0225277.
2000US-0225778.
2000US-0225778.
2000US-0225778.
2000US-0225778.
2000US-0225778.
2000US-0225778.
2000US-0225778.
2000US-0225778.
2000US-0225778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US01239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
         22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
23-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
14-SEP-2000;
14-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0229509
2000US-0229513
2000US-0230438
2000US-0231242
2000US-0231244
2000US-0231244
2000US-0231414
2000US-0231414
2000US-0232080
2000US-0232080
2000US-0232081
2000US-0232397
2000US-0232397
2000US-0232390
2000US-0232390
2000US-0232390
2000US-0232390
2000US-02323063
2000US-0233063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0226868.
2000US-0227182.
2000US-0227009.
2000US-0228924.
2000US-0229287.
                                                                                                                                                                                                                                                                                                                                  2000US-0235836
2000US-0236367
2000US-0236368
2000US-0236368
2000US-0236369
2000US-0236802
2000US-0237037
2000US-0237037
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
          2000US-0240960

2000US-0241785

2000US-0241786

2000US-0241809

2000US-0241809

2000US-0246174

2000US-0246174

2000US-0246174

2000US-0246474

2000US-0246475

2000US-0246475

2000US-0246477

2000US-0246477

2000US-0246477

2000US-0246477

2000US-0246477

2000US-0246524

2000US-0246524

2000US-0246526

2000US-0246526

2000US-0246528

2000US-0246528

2000US-0246528

2000US-0246613

2000US-0246613

2000US-0246611

2000US-0246611

2000US-0246611

2000US-0246613

2000US-0246613

2000US-0246613

2000US-0246613
```

ý

```
RAGE STATES OF THE STATES OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-
                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 - NOV -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 - NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0251030
2000US-025198
2000US-0256719
2000US-0251479
2000US-0251866
2000US-0251868
2000US-0251869
2000US-0251989
2000US-0251989
2000US-0251990
2000US-0251990
2000US-0251990
2000US-0251997
2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0249208.
2000US-0249209.
2000US-0249211.
2000US-0249211.
2000US-0249213.
2000US-0249214.
2000US-0249214.
2000US-0249215.
2000US-0249217.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249244.
2000US-0249264.
2000US-0249264.
2000US-0249265.
2000US-0249299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249300.
2000US-0250160.
2000US-0250391.
```

Barash SC, Ruben MS,

N-PSDB; 2001-465566/50. AAS41085

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous

Claim 11; SEQ ID No 1211; 1180pp; English.

(e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthitis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 325 AA;

```
Query Match
Best Local Similarity
      Matches 317;
     Conservative
             100.0%; Score 1720; DB 22; 100.0%; Pred. No. 3.3e-147;
     0;
   Mismatches
 Indels
                        Length 325;
0;
Gaps
```

0;

```
AAU17037
ID AAU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                           07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                              04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; vulnerary; secreted protein; cardiovascular disorder; cardiac arrest; hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                                                                        cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                       17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                             WO200155441-A2
                                                                                                                                                                                                                                                                                                                                                                                               skin ageing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU17037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU17037 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VGVAMVEPHPVYSWKEGACADIALVRLERSIQFSERVLPIGLPDASIHLPPNTHGWISGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGALRAPSQGSGAAARS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggalrapsqgsgaaars 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt dsggplmcqvdgawllagiiswgegcaernrpgvyislsahrswvekivqgvqlrgraqg}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gsiqdgvplphpqtlqklkvpiidsevcshlywrgagqgpitedmlcagylegerdaclg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \verb|wpwivsiqkngth| heags | \verb|ltsr| wvita a hefk dn lnkpylfsvllgawq lgnpgsrsqk|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vgvawvephpvyswkegacadialvrlersiqfservlpiclpdasihlppnthcwisgw
              2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0215135.
2000US-0216647.
2000US-0216647.
2000US-0217486.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217496.
2000US-0217496.
2000US-0218290.
2000US-0218296.3
2000US-022964.
                                                                                                                                                                                                                                                                                                                                                                                              food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                  2000US-0180628
2000US-0184664
                                                                                                                                                                                                                                                                                       2001WO-US01320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                   2000US-0186350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
```

14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

2000US-0225213
2000US-0225214
2000US-0225266
2000US-0225266
2000US-0225276
2000US-0225775
2000US-022575
2000US-0225759
2000US-0225759
2000US-0225759
2000US-02256816
2000US-02256816
2000US-0225829
2000US-02258924
2000US-02293843
2000US-02293845

22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000;

```
2000US-023239
2000US-0232398
2000US-0232401
2000US-0232401
2000US-0233063
2000US-0234274
2000US-0234274
2000US-0234997
2000US-0235834
2000US-0235834
2000US-0235834
2000US-0235834
2000US-0235836
2000US-0236367
2000US-0236367
2000US-0236369
2000US-0236369
2000US-0236369
2000US-0237039
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0241785
2000US-0241786
2000US-02446476
2000US-0246476
                 The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They CC are also used in diagnosing a pathological condition or susceptibility CC be used in alleviating symptoms associated with the disorders and in CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated cc include autoimmune diseases e.g. rheumatoid arthritis, Cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and fungi C e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or truses and fungi C and control of the breast or liver, C include archaemia, angiogenesis, nervous system disorders e.g. C e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac arrest or liver, C include archaemia, angiogenesis, nervous system disorders e.g. cardiac archaemia, angiogenesis, nervous syst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, haemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-476222/51.
DB; AAS26942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0246523

2000US-0246524

2000US-0246526

2000US-0246527

2000US-0246532

2000US-0246609

2000US-0246611

2000US-0246613

2000US-0249207

2000US-0249209

2000US-0249209

2000US-0249210

2000US-0249211

2000US-0249212

2000US-0249213

2000US-0249213

2000US-0249213

2000US-0249213

2000US-0249213

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214

2000US-0249214
                    disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0251869
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID No 278; 601pp; English.
                    e.g. corneal infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM;
                         and many other
```

 PR

 PR

14-SEP-2000; 14-SEP-2000;

14-SEP-14-SEP-14-SEP-

26-SEP-2000; 27-SEP-2000; 27-SEP-2000;

25-SEP-2000; 25-SEP-2000;

14-SEP-2000; 21-SEP-2000;

14-SEP-2000; 14-SEP-2000;

21-SEP-2000;

01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-0233438 2000US-0231242 2000US-0231243 2000US-02312413 2000US-0233413 2000US-0233080 2000US-0232081 2000US-0232081 2000US-0232081 2000US-0232081 2000US-023397

29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 13-CCT-2000; 13-CCT-2000; 20-CCT-2000; 20

ď

88888888

δõ 밁 Qy

```
RESULT
AAU16966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capabilities, fat content, lipid, protein, carbohydrate, vitamins minerals, cofactors and other nutritional components. The present
                  24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                 cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                   Cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel secreted protein, SEQ ID 207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU16966 standard; Protein; 351 AA.
                                                                                        31-JAN-2000;
04-FEB-2000;
                                                                                                                                            17-JAN-2001;
                                                                                                                                                                                02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2001
                                                                                                                                                                                                                 WO200155441-A2.
                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129
                                                                                                                                                                                                                                                                                                                                                                                                                              uman; immunosuppressive; antiarthritic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGALRAPSQGSGAAARS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
2000US-0179065.
2000US-0184664.
2000US-0184564.
2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                            2001WO-US01320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1720; DB 22; Pred. No. 3.3e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
       14-AUG-2000

14-AUG-2000

14-AUG-2000

18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
     14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0225213

2000US-0225267

2000US-0225267

2000US-0225267

2000US-0225758

2000US-0225757

2000US-0225759

2000US-0225759

2000US-0225759

2000US-0225718

2000US-0226681

2000US-022668

2000US-0227182

2000US-0227182

2000US-0227183

2000US-0229343

2000US-0229343

2000US-0229343

2000US-0229343

2000US-0229343

2000US-0231244

2000US-0231243

2000US-0231243

2000US-0231243

2000US-0231243

2000US-0231243
                            2000US-0231414
2000US-0231080
2000US-0232081
2000US-0232397
2000US-0232397
2000US-0232399
2000US-0232401
2000US-0232401
2000US-023363
2000US-023363
2000US-0234274
2000US-0234274
2000US-0234274
2000US-0234294
2000US-0234294
2000US-0234294
2000US-0234363
2000US-0235834
2000US-0235834
2000US-0235836
2000US-0235836
2000US-0235836
2000US-0235836
2000US-0236370
2000US-0237038
2000US-0237038
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
2000US-0237039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0216880
2000US-0217487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0215135.
2000US-0216647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0205515.
2000US-0209467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0224518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0217496.
2000US-0218290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-022451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0220964
```

밁 Qy 밁 δÃ Вþ γ 뮹

XXXX

Page

```
        PR

                                                                                                                                                                                                                                                                                                                                 08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8-NOV-2000;
                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                    08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NOV-2000;
                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0249215.

2000US-0249216.

2000US-0249217.

2000US-0249218.

2000US-0249214.

2000US-0249244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0249264.
2000US-0249265.
2000US-0249297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0249208.
2000US-0249209.
2000US-0249210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0241221.
2000US-0241785.
2000US-0241786.
2000US-0241787.
2000US-0241808.
2000US-0241808.
2000US-0241826.
2000US-0241826.
2000US-0244617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0246478.
2000US-0246523.
2000US-0246524.
2000US-0246525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0246475.
2000US-0246476.
2000US-0246477.
                                                                                                                                                                                                                                                                                                   2000US-0251990
                                                                                                                                                                                                                                                                                                                                               2000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0249213.
2000US-0249214.
                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0250391
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0249300.
2000US-0250160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0249299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0249211.
2000US-0249212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0246613.
2000US-0249207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0246610.
2000US-0246611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0246609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0246526.
2000US-0246527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0246474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0246528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246532.
                                                                                                                                                                                                      SM;
```

diagnose discactivity of phaemophilia Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,

N-PSDB; AAS26871. WPI; 2001-476222/51.

Claim 11; SEQ ID No 207; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used and proteins are used to

02-AUG-2001

i

```
RESULT 10
AAU23751
ID AAU237
Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δã.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They CC are also used in diagnosing a pathological condition or susceptibility CC to a pathological condition. Antibodies to the proteins can also CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated CC include autoimmune diseases e.g. rheumatoid arthritis, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other CC Alzheimer's disease, infections caused by bacteria, viruses and fungicand coular disorders e.g. corneal infection, and many other collar disorders e.g. corneal infection. The polypeptides can also CC disorders listed in the specification. The polypeptides can also CC be used to aid wound healing and epithelial cell proliferation, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                       Human; oxidoreductase enzyme; transferase; hydrolase; lyase; is
ligase; hyperproliferative disorder; immunodeficiency disorder;
autoimmune disorder; neurological disorder; metabolic disorder;
inflammatory disorder; cardiovascular disorder; reproductive disorder-
blood-related disorder; infectious disorder; cytostatic; anti a
                                                                                                                       nephrotropic; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                             18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               AAU23751 standard;
                                                                                                                                                                                                                                                                   Novel human enzyme polypeptide #837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevent skin aging due to sunburn, to maintain organs before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 ggalrapsqgsgaaars 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GGALRAPSQGSGAAARS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gsiqdgvplphpqtlqklkvpiidsevcshlywrgagqgpitedmlcagylegerdaclg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vgvawvephpvyswkegacadialvrlersiqfservlpiclpdasihlppnthcwisgw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wpwivsiqkngthhcagslltsrwvitaahcfkdnlnkpylfsvllgawqlgnpgsrsqk 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1720; DB 22; 100.0%; Pred. No. 3.6e-147; cive 0; Mismatches 0;
                                                                                                                                                          reproductive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                            isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274
```

0

```
01-SEP-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
14-SEP-2000
25-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
27-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2000
30-JUN-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
14-JUL-2000
6-JUL-2000
14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001;
       2000US-0229343
2000US-0229343
2000US-0229343
2000US-0229343
2000US-0229343
2000US-0229433
2000US-0231243
2000US-0231243
2000US-0231243
2000US-0231413
2000US-0231413
2000US-0231414
2000US-0231413
2000US-0232081
2000US-0232081
2000US-023297
2000US-0232397
2000US-0232397
2000US-0232397
2000US-0232401
2000US-0232401
2000US-0232401
2000US-0233404
2000US-0233404
2000US-0233404
2000US-0233404
2000US-0234984
2000US-0234984
2000US-0235834
2000US-0235834
2000US-0235834
                                                                                                                                                                                                                                                                                                                                                                                                                2000US-022963
2000US-0229518
2000US-0224518
2000US-0224519
2000US-0225213
2000US-0225214
2000US-022526
2000US-022526
2000US-022526
2000US-022527
2000US-022547
2000US-0225757
2000US-0225758
2000US-0225759
2000US-0226868
2000US-0226868
2000US-0226868
2000US-0227182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0179065.
2000US-018628.
2000US-0186350.
2000US-0186350.
2000US-0198123.
2000US-0198123.
2000US-0205515.
2000US-0205515.
2000US-0216886.
2000US-0216886.
2000US-0216880.
2000US-0217487.
2000US-0217487.
2000US-0217487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US01239.
  17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-2000
29-SEP-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000
13-OCT-2000
13-OCT-2000
20-OCT-2000
01-NOV-2000
08-NOV-2000
WPI; 2001-465566/50.
N-PSDB; AAS41621.
                               Rosen CA,
                                                       ( HUMA - )
                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                              L7-NOV-2000;
                                                       HUMAN GENOME
                               Barash SC,
                                                                          2000US-0249211
2000US-0249213
2000US-0249213
2000US-0249214
2000US-0249214
2000US-0249214
2000US-0249216
2000US-0249245
2000US-0249264
2000US-0249264
2000US-0249264
2000US-0249264
2000US-0249269
2000US-0249269
2000US-0259160
2000US-0259186
2000US-0251868
2000US-0251869
2000US-0251869
2000US-0251899
2000US-0251999
                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0241785.
2000US-0241786.
2000US-0241809.
2000US-0244617.
2000US-0244617.
2000US-0246474.
2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246523.
2000US-0246524.
2000US-0246526.
2000US-0246527.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246529.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246610.
2000US-0246610.
2000US-0246611.
2000US-0249208.
2000US-0249208.
2000US-0249208.
2000US-0249208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0237038
2000US-0237039
2000US-0237040
2000US-0239935
2000US-0239935
2000US-0239937
2000US-0240960
2000US-0241221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0236369.
2000US-0236370.
2000US-0236802.
2000US-0237037.
                                                       SCI INC
                                 SM;
```

```
Pr Novel polypeptides and polynucleotides useful for diagnosing, Pr preventing, treating neural, immune system, muscular, reproductive, Pr pulmonary, cardiovascular, renal, proliferative disorders and cancerous Pr diseases.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Claim 11; SEQ ID No 1747; 1180pp; English.

XX Sequence 322 AA;

XX Sequence 322 AA;
```

QΥ 망 В οy В δÃ Š В Qy В Query Match Best Local S Matches 316 186 gsiqdgvplphpqtlqklkvpiidsevcshlywrgagqgpitedmlcagylegerdaclg 245 181 GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG 240 301 GGALRAPSQGSGAAARS 317 66 61 WPWIVSIOKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWOLGNPGSRSOK 120 Local Similarity 99.7 les 316; Conservative 6 mvvsgappalgggclgtftsllllastailnaaripvppacgkpqqlnrvvggedstdse 65 1 MYVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE 60 ggalrapsqgsgaaars 322 99.7%; 99.7%; 0; Mismatches Score 1714; DB 22; pred. No. 1.1e-146; Length 322; Indels 0; Gaps 0

Search completed: August 13, 2002, 08:47:16 Job time: 244 sec

```
Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                 554
538.5
538.5
530.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
522.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
622.5
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              607.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
      August 13, 2002, 08:45:47; Search time 17.42 Seconds (without alignments) 1748.583 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVVSGAPPALGGGCLGTFTS.....AQGGGALRAPSQGSGAAARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-040-803-7
1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pir1:*
pir2:*
pir3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pir4:*
      B
      PLPG
PLHU
T30337
A47547
A56318
A43090
A32869
B61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A57014
A38654
A32410
JC4171
S68702
A45754
B35863
C35863
C35863
S56160
A47246
KQHUP
                                                                                                                                                                                                                                    KQMSPL
KQRTPL
PLBO
A53663
S00845
S33777
B30848
A61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostasin (EC 3.4. mast cell proteina tryptase (EC 34.2 tryptase (EC 3.4.2 mast cell tryptase t
plasma kallikrein
plasmin (EC 3.4.21
enteropeptidase (E
hepsin (EC 3.4.21,
hepsin (EC 3.4.21,
plasmin (EC 3.4.21)
polyprotein Afri
serine proteinease
enteropeptidase (E
enteropeptidase (E
apolipoprotein(a)
plasmin (EC 3.4.21)
                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation factor plasma kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
```

Query Match Query Match Query Match Best Local Similarity 44.2%; Pred. No. 6.3e-44; Best Local Similarity 44.2%; Pred. No. 6.3e-44; Matches 129; Conservative 42; Mismatches 108; Indels 13; G. Qy 10 LGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVS	A;Generics: A;Generics: A;GenericBH:PRSS8 A;Cross-references: GDB:676446; OMIM:600823 A;Map position: 16p11.2-16p11.2 C;Superfamily: prostasin; trypsin homology C;Superfamily: prostasin; trypsin homology C;Keywords: glycoprotein; hydrolase; serine protein F;1-32/Domain: signal sequence #status predicted <s #status="" <try="" chain="" domain:="" f;33-44="" f;45-343="" heavy="" homology="" light="" predicted="" prostasin="" trypsin=""> F;45-381/Domain: trypsin homology <try> F;37-154,70-86,168-244,201-223,234-262/Disulfide bo F;35,134,238/Active site: His, Asp, Ser #status pred F;159/Binding site: carbohydrate (Asn) (covalent) #</try></s>	RESULT 1 A57014 A57014 A57014 Prostasin (EC 3.4.21) precursor - human C;Species: Homo sapiens (man) C;Accession: A57014; Moin secific expression, and cellul spiritie: Molecular cloning, tissue-specific expression, and cellul A;Reference number: A57014; MOID:95286644 A;Ritle: Molecular cloning tissue-specific expression, and cellul A;Reference number: A57014; MOID:95286644 A;Accession: A57014 A;Accession: A57014 A;Accession: A57014 A;Cross-references: GB:L41351; NID:9862304; PIDN:AAC41759.1; PID:9A;Experimental source: prostate A;Note: parts of this sequence were determined by protein sequenci R;Yu, J.X.; Chao, J. J. Biol. Chem. 269, 18843-184848, 1994 A;Title: Prostasin is a novel human serine proteinase from seminal A;Accession: A54866 A;Molecule type: protein A;Residues: 45-64 < YUA>	30 439.5 25.6 812 1 PLMS 31 437.5 25.4 437 2 JEO114 32 437.5 25.4 4548 1 SO0657 33 437.5 25.4 4548 1 SO0657 34 437 25.4 263 1 KYRTB 35 437 25.4 421 1 S11674 36 434 25.2 271 2 A25528 37 433.5 25.1 436 2 JYO172 38 432.5 25.1 436 2 JYO172 39 430.5 25.0 366 2 JEO105 40 429.5 25.0 431 2 S47538 41 428 24.9 263 2 A21195 42 425 24.7 270 2 B2994 44 422 24.5 415 1 A34170 ALIGNMENTS
1; Length 343; 18; Indels 13; Gaps 7; NRYVGGEDSTDSEWPWIVS 66 : :	se; transmembrane protein <pre> AMATS ted <chl> cted <chh> mM1> ds: #status predicted icted icted tatus experimental</chh></chl></pre>	<pre>Lext_change 18-Jun-1999 on, and cellular localization of 41759.1; PID:g862305 otein sequencing e from seminal fluid. Purificatio</pre>	plasmin (EC 3.4.21 testicular serine acrosin (EC 3.4.21 apoprotein(a) (EC chymotrypsin (EC 3 acrosin (EC 3.4.21 hypothetical prote pancreatic elastas acrosin (EC 3.4.21 testicular serine acrosin (EC 3.4.21 chymotrypsin (EC 3.4.21 pancreatic elastas chymotrypsin (EC 3.4.21 pancreatic (EC 3.4.21 pancreatic (EC 3.4.21

```
Qy
                                                                                                       망
                                                                                                                                                QY
                                                                                                                                                                                                                                                                                                          F;32-31/Domain: activation peptide *status predicted <ACT>
F;32-276/Product: mast cell proteinase 6 *status experimental <MAT>
F;32-268/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser *status predicted
                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 24/1; 79/2; 168/1; 222/3
C:Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson, Scand. J. Immunol. 38, 359-367, 1993
A;Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A35646; MUID:90222202
A;Accession: D35646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 32-54 < RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509 R;Reynolds, D.S.; Stevens, R.I.; Lane, W.S.; Carr, M.H.; Austen, K.F.; St Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990 A;Title: Different mouse mast cell populations express various combinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Molecule: 1-276 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: I59478; MUID:94023807
A;Accession: I59478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g200507 A;Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 3; SG1y, GAG for residue 148 as G1y, GAG for residue 168 as G1y, and GAA for 185 as G1y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B38654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-276 < REY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A38654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A38654
                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Mus musculus (house mouse)
;Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
cession: A38654; B38654; D35646; I59478
nolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
ol. Chem. 266, 3847-3853, 1991
*Tile: Cloning of the cDNA and gene of mouse mast cell protease-6. Transc:
;Reference number: A38654; MUID:91139682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   éne: MMCP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    idues: 1-276 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s-references:
              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 GPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 EPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG 186
                                                         77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                             21 LLLLASTAILNAARIPVP-PACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCA 76
                                                                                                                                                                                                                      Local Similarity
                                                                                                       6
                                                  GSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQL--GNPGSRSQKVGVAWVEPHPVYSW 134
       GSLIHPQWVLTAAHCVGPHIKSPQLFRVQLREQYLYYGD-----QLLSLNRIVVHPHYYT 116
                                                                                                  LLLLWALSLLASLYYSAPRPA----NQRVGIVGGHEASESKWPWQVSLRFKLNYWIHFCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPLPHPQTLQKLKVPIIDSEVCSHLYWRGA-GQGP--ITEDMLCAGYLEGERDACLGDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKVTELQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGKDACQGDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPHPSY-LQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPS 179
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:L31853; NID:g473480;
                                                                                                                                                                                                                      32.2%;
                                                                                                                                                                                              48;
                                                                                                                                                                                                              Score 554; DB 2;
Pred. No. 1.7e-39;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN: AAA39725.1;
                                                                                                                                                                                              93;
                                                                                                                                                                                                                                      Length 276;
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g473481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
                                                                                                                                                                                           22;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serafin, W.E.
                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                     R; Ide, H.; Itoh, H.; Tomita, M
J. Biochem. 118, 210-215, 1995
A; Title: cDNA sequencing and ex
                                                                   C; Accession:
R; Ide, H.; It
                                                                                                            tryptase (EC 3.4.21.59) precursor - rat N;Alternate names: mast cell tryptase C;Species: Rattus norvegicus (Norway rat) C;Date: 27-Aug-1995 #sequence_revision 27
                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                         δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
A32410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Vanderslice, P.; Craik, C. Biochemistry 28, 4148-4155,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112;
                                                                                             JC4171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                   H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama,
JC4171; M
d expression of MUID:96015171
```

```
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-30/Domain: activation peptide #status predicted <ACT:F;31-275/Product: tryptase #status predicted <MAT>F;31-267/Domain: trypsin homology <TRY>F;74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning of dog mast cell tryptase and a related A;Reference number: A32410; MUID:89352460
A;Accession: A32410
A;Molecule type: mRNA
A;Residues: 1-275 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: trypsin; trypsin homology C; Keywords: hydrolase; serine proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tryptase (EC 3.4.21.59) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 11-oct-1989 #sequence_revision
C;Accession: A32410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M24664; NID:g163982; PIDN:AAA30854.1;
238 QAGVVSWGEGCAQPNRPGIYTRVAYYLDWIHQYV 271
                                                         256 LAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 KEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG---THHCAGSL
                                                                                                                            VPIVENSMCDVQYHLGLSTGDGVRIVREDMLCAG--NSKSDSCQGDSGGPLVCRVRGVWL
                                                                                                                                                                                             VPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWL 255
                                                                                                                                                                                                                                                                    ADIALLELEDPVNVSAHVQPVTLPPALQTFPTGTPCWVTGWGDVHSGTPLPPPFPLKQVK 179
                                                                                                                                                                                                                                                                                                                                    ADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEGAC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVLALALLGSL-VPVSPAPGQALQRVGIVGGREAPGSKWPWQVSLRLKGQYWRHICGGSL 63
                                                                                                                                                                                                                                                                                                                                                                                                    IHPQWVLTAAHCVGPNVVCPEEIRVQLREQHL---YYQDHLLPVNRIVMHPNYYTPENG- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGTWLQAGVVSWGEGCAQPNKPGIYTRVTYYLDWIHRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEGG-ADVALLELEVPVNVSTHIHPISLPPASETFPPGTSCWVTGWGDIDNDEPLPPPYP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKQVKVPIVENSLCDRKYHTGLYTGDDFPIVHDGMLCAG--NTRRDSCQGDSGGPLVCKV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQKLKVPIIDSEVCSHLYWRGAGQG---PITED-MLCAGYLEGERDACLGDSGGPLMCQV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craik, C.S.; Nadel, J.A.; Caughey, G.H.
148-4155, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 546; DB 2
Pred. No. 8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-Oct-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g163983; GB:J02862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease: structur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
```

27-Oct-1995 #text_change 20-Jun-2000

Osada,

rat mast cell tryptase

```
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase;
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID:g556556 C;Comment: This enzyme is basically specific for a connective tissue mast cell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JC4171
A; Molecule type: mRNA
A; Residues: 1-274 <IDE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;20-29/Domain: activation peptide #status predicted <ACTP F;30-274/Product: mast cell tryptase #status predicted <MATP F;30-266/Domain: trypsin homology <TRYP F;73,120,223/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      einase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;73,120,223/Active site: His, Asp, Ser *status predicted F;131/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                 A; Accession: $68676

A; Molecule type: protein
A; Mcsidues: 'IVGGGEAP',1-8;61-74;90-97;126-148;162-190;208-222;227-235 <PAW>
A; Residues: 'IVGGGEAP',1-8;61-74;90-97;126-148;162-190;208-222;227-235 <PAW>
C; Superfamily: trypsin; trypsin homology
C; Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
C; Reywords: glycoprotein; hydrolase; serine proteinase; zymogen
C; Reywords: glycoprotein; homology (fragment) <TRY>
F; 36, 83, 177/Active site: His, Asp. Ser #status predicted
F; 94, 195/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tryptase (EC 3.4.21.59) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-237 < PAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: $68676; MUID: 96203914
A; Accession: $68702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S68702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
В
                                            ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X94982; NID:g1332446; PIDN:CAA64438.1; PID:g1332447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laoro, M.; Gambacurta, A.; Fiorucci, L.; Mignogna, G.; Barra, D.; Ascoli, F. J. Biochem. 237, 100-105, 1996
Lie: cDNA cloning and primary structure of tryptase from bovine mast cells, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ession: S68702; S68676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 DEPLLPPYPLKQVKVPIVENSLCDRKYHTGLYTGDDVPIVQDGMLCAG--NTRSDSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQG---PITED-MLCAGYLEGERDACLGD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 VHPH-YYTVEDG--ADIALLELEIPVNVSTHIHPISLPPASETFPSGTSCWVTGWGDIDS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 LLLLAST---AILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGT---HH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 CGGSLIHPQWVLTAAHCVGLHIKSPELFRVQL-----REQYLYYADQLLTVNRTV 107
                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LLLLALSPLASLVHAAPCPVKQRVG-----IVGGREASESKWPWQVSLRFKFSFWMHF 57
                                                                                                                       Local
  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQ------KVGVAW 125
                               SEWPWIVSI---QKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGPLVCKVKGTWLQAGVVSWGEGCAEANRPGIYTRVTYYLDWIHRYV 270
  SQWPWQVSLRVSRRYWRHHCGGSLIHPQWVLTAAHCVGPEVHGPSYFRVQLREQHL---Y 58
                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.3%;
                                                                                                                       31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 538.5; DB 2;
Pred. No. 3.4e-38;
                                                                                                  Score 536; DB 2;
Pred. No. 4.7e-38;
8; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     evid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
            밁
                                                      Ş
                                                                                                          밁
                                                                                                                                                      γQ
                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                     δð
                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
```

```
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
C;Accession: A45754; B37193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: hydrolase; serine proteinase; zymogen
E;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted </R
E;31-274/Product: tryptase I #status predicted <MAT>
F;31-266/Domain: trypsin homology <TRY>
F;74,120,223/Active site: His, Asp, Ser #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human tryptas A;Reference number: A37193; MUID:90369005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
J. R;Title: Cloning and Miller of Complementary DNA for human tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-274 < MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the sequence from Fig. 4 is inconsistent with that from C; Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-274 <MI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A45754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A45754; MUID: 90009311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptase (EC 3.4.21.59) alpha precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB:M30038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B37193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:M30038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 QG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 SRSQKVGVAWVEPHP-VYSWKEGACADIALVRLERSIQESERVLPICLPDASIHLPPNTH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 QG
                                                                                                                                                                                                                  113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                      248
                                                                                                         171
                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 SLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt CWVTGWGNVDNGRRLPPFFLKQVKVPVVENSVCDRKYHSGLSTGDNVPIVREDMLCAG-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQDQLLPISRIIPHPNCYSVKNG--ADIALLELDKLVNISWHVQPVTLPPESETFPPGTQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DSGRNFCQGDSGGPLVCKVNGTWLQAGVVSWGDGCAKPNRPGIYTRVTSYLDWIHQYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt LEGERDACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV-}
                                                                                                                                                                                                                                                                                                                                                                            GSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGS----RSQKVGVAWVEPHP-V 131
CKVNGTWLQAGVVSWDEGCAQPNRPGIYTRVTYYLDWIHHYV 270
                                                                                                                                                         PQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGDSGGPLM 247
                                                                                                                                                                                                               YIIQTG--ADIALLELEEPVNISSRVHTVMLPPASETFPPGMPCWVTGWGDVDNDEPLPP 170
                                                                                                                                                                                                                                                                  YSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPH 191
                                                      CQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                         PFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDMLCAG--NSQRDSCKGDSGGPLV 228
                                                                                                                                                                                                                                                                                                                           GSLIHPQWVLTAAHCLGPDVKDLATLRV-----NSGTHLYYQDQLLPVSRIMVHPQF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                  SLLLLALPVL--ASRAYAAPAPVQALQQAGIVGGQEAPRSKWPWQVSLRVRDRYWMHFCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 532;
40.1%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8,
```

```
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-275 < RES>
A; Cross references: GB:S55551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
A; Experimental source: basophil cell line KU812
C; Genetics:
C; Genetics:
A; Grene: GDB:TPS1
A; Cross -references: GDB:125890; OMIM:191080
A; Map position: l6pter-16qter
C; Keywords: hydrolase; serine proteinase; zymogen
C; Keywords: hydrolase; serine proteinase; zymogen
C; Keywords: hydrolase; serine proteinase; zymogen
                                                         δõ
                                                                                                                                                                      20
                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
      Db
                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                      Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;22-30/Domain: activation peptide #status predicted <ACT>F;31-275/Product: tryptase I #status predicted <MAT>F;31-267/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Blom, T.; Hellman, L. Scand. J. Immunol. 37, 203-208, 1993
A;Title: Characterization of a tryptase mRNA expressed in A;Reference number: I59473; MUID:93166209
A;Accession: I59473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983
A;Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic R;Miller, J.S.; Moxley, G.; Schwartz, L.B.
J_Clin. Invest. 86, 864-870, 1990
Le: Cloning and characterization of a second complementary DNA for human tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: B35863; A37193; I59473
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A;Reference number: A35863; MUID:90251647
A;Accession: B35863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-275 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA; DNA
A; Residues: 1-275 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Alternate names: tryptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tryptase (EC 3.4.21.59) II precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erence number: A37193; MUID:90369005 ession: A37193
         224
                                                            242
                                                                                                                      166
                                                                                                                                                                   186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD
                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                127 EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y Match
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 SLLLLASTATINAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG---THHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NLLLLALPVL--ASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCG
                                                                                                                                                                                                                                                                                                                                                                                                 GSLLTSRWVITAAHC----FKD-----NLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV 126
SGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYV
                                                   SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                             DERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGD
                                                                                                                                                                                                                             IVHPQFYTAQIG--ADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDN 165
                                                                                                                                                                                                                                                                                                                                                GSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%; Score 530.5; DB 2
39.2%; Pred. No. 1.6e-37;
tive 53; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 275;
                                                                                                                                                                                                                                                                                                                                             ---YQDQLLPVSRI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the human basophil cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ର
```

```
C;Superfamily: trypsin; trypsin homology
(;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: trypsin homology <TRY>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted
                                                         Ş
                                                                                                                          B
                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 31-38 <CRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chreti J. Biol. Chem. 262, 1363-1373, 1987
A;Title: Human pituitary tryptase: molecular forms, NH-2-terminal sequence, immunocyt A;Reference number: A39326; MUID:87109258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 31-38,'P',40-41,'X',43,'T',45-48,'X',50 <BUT>
A; Experimental source: mast cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M33491
R;Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roc
J. Leukoc. Biol. 47, 409-419, 1990
A;Title: Purification of tryptase from a human mast cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (mān)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C;Accession: A35863; D35863; A60939; A39326
R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A;Reference number: A35863; MUID:90251647
A;Accession: A35863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 21/1; 78/2; 177/1; 221/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A60939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A60939; MUID: 90244210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-275 < VA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-275 <V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tryptase (EC 3.4.21.59) I precursor - human
C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A39326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: D35863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
      224
                                                                242
                                                                                                                      166 DERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGD
                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                             108 IVHPQFYTAQIG--ADIALLELEEPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDN
                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 SLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG---THHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NILLLALPVI--ASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44-Gly was also found
                                SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV
SGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYV 271
                                                                                                                                                                             GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD
                                                                                                                                                                                                                                                                                                       EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                                 GSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLY------YQDQLLPVSRI 107
                                                                                                                                                                                                                                                                                                                                                                                                                              GSLLTSRWVITAAHC----FKD-----NLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.8%; Score 529.5; DB 2; Length 275; 39.2%; Pred. No. 2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.R.; Roche,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9:
```

9;

```
mast cell tryptase precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 27-Oct-1955 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Accession: S56160
R;Murakumo, Y; Ide, H; Itoh, H; Tomita, M.; Kobayashi, T.; Maruyama, H; Horii, Y.; |
Biochem. J. 309, 921-926, 1995
A;Title: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones |
A;Reference number: S56160; MUID:95366971
A;Accession: S56160
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-270 <MUR>
A;Cross-references: EMBL:D31789; NID:9517122; PIDN:BAA06598.1; PID:9517123
C;Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erence number: A38893

ssion: A38893

cule type: mRNA

A;Cross:references: GB:M33493; NID:g339984; PIDN:AAA36780.1; PID:g339985

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; serine proteinase; zymogen

F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase I #status predicted <AACT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tryptase (EC 3.4.21.59) III precursor - human C;Species: Homo sapiens (man) C;Date: 03.7eb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Jun-2001 C;Accession: C35863; A35863; A38893 R;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990 A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr A;Reference number: A35863; MUID:90251647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to GenBank, April 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Vanderslice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
A;Note: the first nine residues of this sequence are inferred from genomic DNA of trypta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: C35863
A; Molecule type: mRNA
A; Residues: 9-275 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A35863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA Residues: 1-9 <VA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 IVHPQFYTAQIG--ADIALLELEEPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 DERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GSLIHPQWVLTAAHCVGFDVKDLAALRVQLREQHLY------YQDQLLPVSRI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GSLLTSRWVITAAHC----FKD-----NLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 SILLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NLLLLALPVL--ASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVRDRYWMHFCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 522.5; DB : Pred. No. 7.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
```

F;26-262/Domain: trypsin homology <TRY>

```
οy
                                                                                                                                                                                 망
                                                                                           Ъ
                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                    162 VSLPPPFPLKEVQVPVVENQLCDLKYHKGVYTGDNIHIVRDDMLCAGN-EG-HDSCQGDS
220 GGPLVCKVNGTWLQAGVVSWGEGCALPNRPGIYTRVTYYLDWIHRYV 266
                                       243 GGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                           187 VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGDS
                                                                                                                                                                        104 THPTFYATQNG--ADIALLELKNPVNISSHVHPVSLPPASETFPSGTLCWVTGWGNIDND 161
                                                                                                                                                                                                               128 PHPV-YSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG 186
                                                                                                                                                                                                                                                                57 SLIHPOWVLTAAHCVGPTIADPNKVRVQLRKQYLY--
                                                                                                                                                                                                                                                                                                        78 SILTSRWVITAAHC-----FKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVE 127
                                                                                                                                                                                                                                                                                                                                                                                              21 LLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGT---HHCAG 77
                                                                                                                                                                                                                                                                                                                                                    4 LLLLALPLESLMHRSPLCQEWG-----IVGGQEAPGNKWPWQVSLRANETYWRHFCGG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 522; DB 2; Length 270; Pred. No. 8.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                             84; Indels
                                                                                                                                                                                                                                                                ----YHDHLLAVSRII 103
                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                242
```

Search completed: August 13, 2002, 08:48:00 Job time: 133 sec

• / • /

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run
                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                      MInimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on:
 ched:
                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                             number of hits satisfying chosen parameters:
Score
Query
                                                                                                                                                                                                                                                                                                                          SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                            105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-040-803-7
1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVVSGAPPALGGGCLGTFTS.....AQGGGALRAPSQGSGAAARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             August 13, 2002, 08:47:37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                          Length DB
BSS4_HUMAN
BSS4_MOUSE
MPN_HUMAN
PSS8_HUMAN
PSS8_RAT
        TRYG_MOUSE
MCT7_MOUSE
TMS5_HUMAN
KAL_HUMAN
FA11_HUMAN
FA11_HUMAN
KAL_MOUSE
TMS4_HUMAN
KAL_ROUSE
TMS4_HUMAN
KAL_RAT
HEPS_MOUSA
TMS3_HUMAN
KAL_RAT
HEPS_MOUSA
TMS9_HUMAN
PLMN_BOVIN
                                                                                                      TRYG_HUMAN
MCT6_MOUSE
TRYT_CANFA
MCT6_RAT
TRYT_PIG
TEST_HUMAN
TRB2_HUMAN
TRB1_HUMAN
TRYA_HUMAN
TRYA_HUMAN
TRYA_HUMAN
TRYA_HUMAN
TRYA_HUMAN
TRYA_HUMAN
TRYA_HUMAN
                                                                                                                                                                                               TRYT_SHEEP
PSS8_MOUSE
                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search time 13.48 Seconds (without alignments) 910.541 Million cell updates/sec
                                                                                                                                                                                                                    Q9gzn4 homo sapien
Q9er10 mus musculu
Q9bqr3 homo sapien
Q16651 homo sapien
       P14272
035453
015393
P06868
                                                   Q9y6m0
P20231
Q9jh231
Q9jh317
Q15661
P15157
P503452
P204417
Q9q417
Q9q417
Q9er04
Q9er04
Q9er04
Q9er05
Q9h3s3
P03952
P2626262
                                                                                                                                                         Q9xsm2
Q9esd1
Q9nrr2
P21845
P15944
P50343
Q9n2d1
                                                                                                                                                                                                              Q9es87
                                                                                                                                                                                                                                                          Description
                                                                                                      3 rattus norv
1 sus scrofa
0 homo sapien
1 homo sapien
7 mus musculu
1 homo sapien
7 homo sapien
7 homo sapien
8 meriones un
5 rattus norv
             homo sapien
rattus norv
mus musculu
homo sapien
                                                  mus musculu
mus musculu
mus musculu
homo sapien
homo sapien
homo sapien
mus musculu
                                                                                                                                                                                             homo sapien
homo sapien
rattus norv
ovis aries
mus musculu
                                                                                                                                                                         mus musculu
canis famil
                                                                                                                                                                                        homo sapien
```

ENTK_PIG

sus scrofa

DR

PROSITE; PS50240; TRYPSIN_DOM; 1.

45	44	43	42	41	40	39	38	3 7	36	35	34
443.5	444	445	445	446	446	446	450	450	451.5	452	453.5
25.8	25.8	25.9	25.9	25.9	25.9	25.9	26.2	26.2	26.2	26.3	26.4
1035	1019	786	333	810	790	338	810	416	855	417	490
1	Н	₽	ب	۲	<u></u>	ш	ш	ш	ш	ш	1
ENTK_BOVIN	ENTK_HUMAN	STUB_DROME	PLMN_CANFA	PLMN_HUMAN	PLMN_PIG	PLMN_HORSE	PLMN_MACMU	HEPS_RAT	ST14_MOUSE	HEPS_HUMAN	TMS2_MOUSE
		Q05319 drosophila									

ALIGNMENTS

	ב א מ	DR	DR	DR	DR	DR	DR	DR	S	CC	 36	3 6	3	င္ပ	S	င္ပ	ය	င္ပ	റ്റ	RL	RA	RA	RA	RA	RP	RN	RL	RT	RT	RA	RC	RP	RN	RL	RT	RT.	RA	RC.	RP	RN	o x	8	റ്റ	SO	GN	DE	ad	D.	ָּבְּלָם בּיִבְּלָם	DI C	אַ הַ	BS	1 R
DESCRIPTION DESCRIPTION OF THE PROPERTY OF THE			InterPro; IPR001254;		MEROPS; S01.252	EMBL; AC003965; AAB93671.1;	EMBL; AF321182; AAG35070.1;	EMBL; AB010779;		or send an email to license@isb~sib.ch).	ווויטבוובט מווע נוודס פרטיפווניו בפ וויסר ופוויסיפטי	modified and this statement is not removed. Hears by and for commerc	use by non-profit institutions as long as its content is in no		between the Swiss Institute of Bioinfor					Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.		Goodwin L., Bryant J., Tesmer J., Meincke L., Long	Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,	Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C	SEQUENCE OF 47-317 FROM N.A.			proteases.";	"Identification of	Wong G.W., Stevens R.L.;	TISSUE=Pancreas;				protease, hBSSP-4.";	"Cloning	Mitsui S., Okui A., Kominami K.,	TISSUE=Brain;			NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhin	Eukaryota; Metazoa; Chordata;	Homo sapiens (Human		(SP001LA).	Brain-specific serine prote	16-OCT-2001 (Rel. 40, Last	16-OCT-2001 (Rel. 40,	16-OCT-2001 (Rel. 40,	09GZN4: 043342:	S4_HUMAN	

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOUTH TO SERVING SOUTH SERVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tches
                                                                                                               TISSUE-Brain;
Mitsui S., Okui A., Kominami K., Yamaguchi N.;
Mitsui S., Okui A., Kominami K., Yamaguchi N.;
"Cloning and characterization of a novel serine protease, mBSSP-4.";
"Cloning and characterization of a novel serine protease, mBSSP-4.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ atabases.
                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
BSS4_MOUSE
D9ER10;
16-OCT-2001
16-OCT-2001
  the Europuse by modified
                                                          This SWI
                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Brain-specific serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE
s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGALRAPSQGSGAAARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGALRAPSQGSGAAARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00134;
PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33
90
141
242
75
175
208
238
238
70
70
47
                                                                                                                                                                                                                                                                                                                                                                                                       Rel. 40,
1 (Rel. 40,
1 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN_HIS; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
317
90
141
242
248
248
248
266
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
protease 4 precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.

BRAIN-SPECIFIC SERINE PROTEASE 4
CHARGE RELAY SYSTEM (BY SIMILARI:
CHARGE RELAY SYSTEM (BY SIMILARI:
CHARGE RELAY SYSTEM (BY SIMILARI:
BY SIMILARITY.
CHARGE GICINGC. . .) (POTENTIAL
L -> M (IN REF. 3).

MM; EZA123BC86E79935 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1720; DB 1;
Pred. No. 2.6e-141;
                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306
                  There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  3.4.21.-) (BSSP-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Mus
  and
                                                          ngh a collaboration EMBL outstation -
  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                        Mus
  commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                     no
no
                  its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

Ų

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB010778; BAB20262.1; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_ERE; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               _HUMAN
                                                  [1]
SEQUENCE FROM Property Management of Man
                                                                                                                                                                                                                                                                                                                                                                                                    MPN_HUMAN
Q9BQR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
SIGNAL
                                                                                                                                                                                      MPN.
Homo sapiens (Human).
Chordata;
                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                     Marapsin
                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seg
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       Fortunato M., Dando P.M., "Cloning, sequencing and
                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSGGPLMCQVDDHWLLTGIISWGEGCAD-DRPGVYTSLLAHRSWVQRIVQGVQLRGYLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGVAMVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGIAWVLPHPRYSWKEGTHADIALVRLEHSIQFSERILPICLPDSSVRLPPKTDCWIAGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPWIVSILKNGSHHCAGSLLTNRWVVTAAHCFKSNMDKPSLFSVLLGAWKLGSPGPRSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMISRPPPALGGDQFSILILLVLLTSTAPISAATIRVSPDCGKPQQLNRIVGGEDSMDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302
                                                                                                                                                                                                                                                                                     precursor
  sequencing
e.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
90
141
242
75
175
208
238
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                        (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
306
90
141
242
242
248
248
227
266
                                                                                                                                                                          Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.9%;
                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
C 3.4.21.-).
                          expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.

POTENTIAL.

BRAIN-SPECIFIC SERINE PROTEASE 4.

CHARGE RELAY SYSTEM (BY SIMILARITE CHARGE RELAY SYSTEM (BY SIMILARITE CHARGE RELAY SYSTEM (BY SIMILARITE BY SIM
                                                        Rawlings N.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1270.5;
Pred. No. 1.5e
25; Mismatches
                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                             Of
f
                                                                                                                                                                                                                                                                                                                                                                                                                                    290
                             marapsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; DB 1
                          Barrett A.J.;
arapsin, a hum
                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                             serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
```

```
RESULT 4
PSS8_HUMAN
ID PSS8_HOMAN
ID 01-001
AC Q16651
DT 01-NOV
DT 01-MAR
DE Prostal
GN PRSS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO FITTER FER FITTER FOR FITTER F
                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                  PSS8_HUMAN STANDARD; PRT; 343 AA.
Q16651; Q9UCA3;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ306593; CAC35467.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                      Prostasin
                                                                                                                                                                                                                 244
                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                      124
                                                                                                                                                                                                                                                                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLLLC----FGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 TSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEGACA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 LLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGTHHCAGSLL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY.
                                                                                                                                                                                                                 AGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGG
                                                                                                                                                                                                                                                                                                                              PIIDSEVCSHLYWRGAGQG----PITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLL 256
                                                                                                                                                                                                                                                                                                                                                                        DVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAV
                                                                                                                                                                                                                                                                                                                                                                                                        DIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEQWYLTAAHCFR-NTSETSLYQYLLGARQLVQPGPHAMYARVRQVESNPLYQ-GTASSA
                                                                                                                                                                                                                                                     AGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGG
                                                                                                                                                                                                                                                                                          PIIDTPKCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S01.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit
                    precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290
277
277
124
229
229
214
214
253
253
253
31940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease;
                        (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARAPSIN.

SERIME PROTEASE.

SERIME PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF OTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 739; DB 1; Pred. No. 1.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                   288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                        183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
        TRANSMEM
DOMAIN
DISULFID
        DISULFID DISULFID
                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gland.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Semen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu J.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                              MIM; 600823;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS;
                                                                                                    PROPEP
                                                                                                                                                               PROPEP
                                                                                                                                                                                 SIGNAI
                                                                                                                                                                                                   Transmembrane
```

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning, tissue-specific expression, and cellular localization of human prostasin mRNA.";
J. Biol. Chem. 270:13483-13489(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITS C-TERMINUS.

-!- TISSUE SPECIFICITY: FOUND IN PROSTATE, LIVER, SALIVARY GLAND, KIDNEY, LUNG, PANGREAS, COLON, BRONCHUS AND RENAL PROXIMAL TUBULL CELLS. IN THE PROSTATE GLAND IT MAY BE SYNTHESIZED IN EPITHELIAL CELLS, SECRETED INTO THE DUCTS, AND EXCRETED INTO THE SEMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 269:18843-18848(1994).
-I- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY
-I- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          SMART; SRUCCE PROSITE; PS50240; TRYPSIN_HIS; PROSITE; PS00134; TRYPSIN_HER; PROSITE; PS00135; TRYPSIN_SER; Zyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purification, tissue distribution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu J.X., Chao L., Chao J.; "Prostasin is a novel human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 45-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95286644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00722; CHYMOTRYPSIN. SMART; SM00020; Tryp_SPc; 1. PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC001462; AAH
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L41351; AAC41759.1; -. EMBL; U33446; AAB19071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94308140; PubMed=8034638;
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                     Hydrolase; Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: MEMBRANE-BOUND, SECRETED AFTER CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S01.159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chao L.,
1
30
33
45
323
323
320
45
70
168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH01462.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chao J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7768952;
                                                                                                                                                                                                                                                                     protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                     Zymogen; Signal; Glycoprotein;
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                               POTENT IAL
                                                                                                                                                                        ACTIVATION PEPTIDE. PROSTATIN LIGHT CHA
                                                                        SERINE PROTEASE
                                                                                                                                                PROSTATIN LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteinase from seminal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELD BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUBULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q.
```

```
CCCCCCCCCCCCCTTT RRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
PSS8_R
                                                                                                                                                                                                                                                                                                                                               OX COR DT DT AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSS8_RAT
Q9ES87; (
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                ---
                                                                                                                                                                                                            "Molecular cloning a Submitted (NOV-1999)
                                                                                                                                                                                                                                                                             Adachi M., Kitamura H
Submitted (SEP-1998)
                                                                                                                                                                                                                                                                                         RISSUE=Kidney;
Adachi M., Kitamur
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Prostasin precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 GPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKVTELQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LGGGCLGTFTSLL---LLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                         SIMILARITY).
SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, DISULFIDE BOND (BY SIMILARITY).
SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                    SIMILARITY: BELONGS
                                                                                                                                                                                                FUNCTION: POSSESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σı
                                                                                                         TRYPSIN FAMILY.
                                                                                                                                ITS C-TERMINUS (BY SIMILARITY)
                                                                                                                                                                                                                                        c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMYCAGYVEGGKDACQGDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPLPHPQTLQKLKVPIIDSEVCSHLYWRGA-GQGP--ITEDMLCAGYLEGERDACLGDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPHPSY-LQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE-AYEVKLGAHQLDSYSEDAKVSTLKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGPGQLGAVAILLYLGLLRSGTGAEGAEAP----CGVAPQA-RITGGSSAVAGQWPWQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ER01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
234
85
134
138
238
159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,
                                                                                                                                                                                               and expression of rat prostasin.";
) to the EMBL/GenBank/DDBJ databases.
ESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                             о
К.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262
262
85
134
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36431
                                                                                                                     TO
                                                                                                                                                                                                                                                                          Miyoshi T., Tomita K.; the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                    PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . . ) (POI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 607.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                 There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ); DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                            SECRETED AFTER CLEAVAGE OF
             http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                          ~
                                                                                                                 S1;
                                                                                                                                                                                                                                                                                                                                                        Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108;
                                                                                                                                                                                                                                                                             databases
                                                                                                                    ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                  KNOWN
                         and
                                                                                                                                                                      HELD BY
                                                                 EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
                                                                 a collaboration - MBL outstation
                                                                                                                  AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                         for
                                                                                                                                                                                                (BY
                                                                outstation
                                       1n
                        in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
```

ò

```
RRR RN XXX
                                                                                                                                                                                                                                                                                                                    RESULT
TRYT_SI
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC PROPERTY OF THE PROPERTY OF
                                                                                                                                            TRYT SHEEP STANDARD; PRT; 2/3
09XSM2;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence upda
16-0CT-2001 (Rel. 40, Last annotation up
Tryptase 2 precursor (EC 3.4.21.59).
0vis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                    _SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
CARBOHYD
  Pemberton A.D., Collie D.D.S.,
                                         TISSUE-Abomasum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID ACT_SITE
                                                         SEQUENCE FROM N.A.
                                                                                                                   Mammalia; Eutheria;
Bovidae; Caprinae;
                                                                                                  NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB017638; BAB20281.1; -.
EMBL; AF202076; AAG32641.1; -.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                 245 PIDGLWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHVAELQPRAVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LGTFTSLLLLASTAILNAARI----PVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                      QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGGKDACQGDSGGPLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YR-EEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGQLEALFILLIGLLQ-SRIGADGTEASCGAVIQ-PRITGGGSAKPGQWPWQVSITYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQTLQKLKVPIIDSEVCSHLY-WRGAGQGP--ITEDMLCAGYLEGERDACLGDSGGPLMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHVCGGSLVSNQWVVSAAHCFPREHSKEE-YEVKLGAHQLDSFSNDIVVHTVAQIISHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168
201
234
85
134
238
159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30
45
323
323
320
45
45
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
  McMillan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                      McAleese
                                                                                                                       OVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286
154
86
244
223
262
262
134
134
159
                                                                                                                                   Chordata; Craniat
Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
344
342
340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.0%;
43.0%;
  L.,
                  S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
    Scudamore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 584; DB 1
Pred. No. 3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .
I -> V (IN REF. 1).
A -> V (IN REF. 1).
                                                                                                                                   Craniata; Vertebratactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE (BY PROSTATIN LIGHT CHAIN. PROSTATIN HEAVY CHAIN. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (BY
                  Huntley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5ED1AF05D9213B98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                      update
                                                                                                                                                                                                                                                                                                273
у J.F.,
С.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Glycoprotein;
                                                                                                                                                                                                                  update)
                                                                                                                                                      Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                  ₿
  , Mackellar A.,
Miller H.R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   بر
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 342
                                                                                                                                       Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                       Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                 295
                                                                                                                                                                                                                                                                                                                                                                                                                                        299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
```

```
CCCCCCCCCCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                               δÃ
                                                                  DЬ
                                                                                                 Š
                                                                                                                                      B
                                                                                                                                                                   Ωy
                                                                                                                                                                                                          В
                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                              QУ
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                     ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way nodified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314;
InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y18224; CAB41989.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequence of sheep mast cell tryptase and its immunolocalisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.143; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                    176
                                                                                                                                                                         138
234
                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                              21 LLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCAG 77
                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung, skin and gut in comparison with sheep mast cell proteinase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-, Lys-1-, but with more restricted specificity than trypsin.

SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ITRYPSIN FAMILY. STRONGEST TO OTHER TRYPTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAST CELL ACTIVATION.
                                  WLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                      G-ADIALLQLEEPVSISRHVQPVTLPPASETFPPESQCWVTGWGDVDNGRPLPPPYPLKQ
                                                                                                                                                                       ACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQK 197
WLQAGVVSWGDGCAKPNRPGIYTRITSYLDWIHQYV
                                                                    VKVPIVENSVCDWKYHSGLSTDYSVPIVQEDNLCAG---DGGRDSCQGDSGGPLVCKVNGT
                                                                                                     LKVPIIDSEVCSHLYWRGAGQG---PIT-EDMLCAGYLEGERDACLGDSGGPLMCQVDGA 253
                                                                                                                                                                                                                                           SLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEG 137
                                                                                                                                                                                                                                                                              LHLLALLLLSL--VSAAPAPGQALQRSGIIGGKEAPGSRWPWQVSLRVRDQYWRHQCGG 59
                                                                                                                                                                                                            SLIHPQWVLTAAHCIGPELQEPSDFRVQLREQHL---YYQDRLLPISRVIPHPHYYMVEN 116
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease;
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        228
209
246
231
                                                                                                                                                                                                                                                                                                                                                                                                                                         30288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                     41.78;
                                                                                                                                                                                                                                                                                                                                                                                     33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Glycoprotein; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                     Score 578.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYPTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATION PEPTIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       -LINKED (GLCNAC. . .) (F
DE9BA79218C3E67D CRC64;
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                       .1e-43
                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                    Length 273;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                           175
                                                                                                                                                                                                                                                                                                                                                    7;
```

δÃ

10 LGGGCLGTFTSLLLLASTAILNAARIP-VPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ 68

-=

..

Query Match Best Local Similarity Matches 124;

33.4%;

Score 574.5; DB 1; Pred. No. 2e-42;

Length 342; Indels

Conservative

46;

Mismatches

110;

11;

Gaps

8

```
RESULT 7
PSS8_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vuagniaux G., Vallet V., Fowler-Jaeger N., Bens M., Farman N., Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E.; "Activation of the amiloride-sensitive sodium channel by the mouse serine protease mCAP1 expressed in a principal kidney cell line."; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases. Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases. "INCLEAVAGE SPECIFICITY (BY SIMILARITY). ACTIVATES AMILORIDE-SENSITIVE SODIUM CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; vercendata; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prostasin precursor (EC 3.4.21.-) (Channel activating protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ESD1;
                                                             ACT_SITE
                                                                                                DISULFID DISULFID
                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                      SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A DISULETDE BOND (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: MEMBERANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRSS8 OR CAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSS8_MOUSE
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1. SMART; SM00020; Tryp_SPc;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF188613; AAG17054.1; ALT_FRAME. InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                          CHAIN
SEQUENCE
                                CARBOHYD
                                                                                                                                  DISULFID
                                                                                                                                                      DISULFID
                                                                                                                                                                     DISULFID
                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                           Hydrolase;
                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50240;
                                                ACT_SITE
                                                                                                                                                                                                                                                                                                            ransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMESHIFT IN POSITION 339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
                                                                                                                                                                                                                                                                                                                           Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
Ā,
                                                                                                                                                                                                                                                                                                                                               TRYPSIN_DOM; 1
36729 MW;
            BY SIMILARITY.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

N-LINKED (GICNAC. . .) (POTENTIAL).

N-LINKED (GICNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         Zymogen; Signal; Glycoprotein;
                                                                                                                                                                                                                                      ACTIVATION PEPTIDE (BY SIMILARITY).
PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
                                                                                                                                                                                                         BY SIMILARITY. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                        SERINE PROTEASE
                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                      INTERCHAIN (BY SIMILARITY).
0620DE88ED187D0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as its content
                                               M (BY SIMILARITY).
M (BY SIMILARITY).
M (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no
```

δÃ В

밁

EMBL; AF223563; AAG48852.2;

```
HIMMAN STANDARD; PRT; 321 AA.

PRYG_HUMAN STANDARD; PRT; 321 AA.

ONRR2; O9NROB; Q9C015; Q9UBB2;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 274:30784-30793(1999).
3]
SEQUENCE OF 220-321 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a new member of the tryptase family of mouse human mast cell proteases which possesses a novel COOH-terminal hydrophobic extension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=99452974; PubMed=10521469;
WONG G.W., Tang Y., Feyfant E., Sali A., Li L.,
Friend D.S., Krilis S.A., Stevens R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
MEDLINE=20302813; PubMed=10843716;
Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M.,
Wolters P.J., Verghese G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of human gamma-tryptases, novel members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     romosome 16p mast cell tryptase and Immunol. 164:6566-6575(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. TRYPTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                               POLYMORPHISM: There are two alleles; differ by 5 residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY:
AF191031;
AF195508;
AF175759;
AF175522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGGKDACQGDSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLPHPQTLQKLKVPIIDSEVCSHLY-WRGAGQGP--ITEDMLCAGYLEGERDACLGDSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDGNHVCGGSLVSNKWVVSAAHCFPREHSREAY--EVKLGAHQLDSYSNDTVVHTVAQII 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THSSYR-EEGSQGDIAFIRLSSPYTFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNGTHHCAGSLLTSRWVITAAHCF-KDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGLGQLEAVTILLLLG--LLQSGIRADGTEASCGAVIQ-PRITGGGSAKPGQWPWQVSIT
; AAF76457.1; -.; AAF76458.1; -.; AAF03697.1; -.; AAF03695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in many tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostasin gene families.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-I and gamma-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
```

밁 Š B δÃ 밁 δÃ

DE RESERVACION CONTRACTOR RESERVACION RESERVACION CONTRACTOR RESERVACION CONTRACTOR RESERVACION RESERVACION RESERVACION RESERVACION RESER

è

GR DI DI AC

MCT6_MOUSE STANDARD; PRT; 276 AA.
P21845; Q61962;
01-MAY-1991 (Rel. 18, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)

Mast cell protease 6 precursor (EC MCPT6.

(MMCP-6) (Tryptase).

```
δÃ
                                                                                              밁
                                                                                                                                      ρ
                                                                                                                                                                                     멍
                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR KKWK KURAN DE PERTET PERTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
TRANSMEM
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; I
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50240;
PROSITE; PS00134;
                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
    232
                                                 252
                                                                                                                                        192
                                                                                                                                                                                     116
                                                                                                                                                                                                                                132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.028
                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                    ω
GAWVQAGIVSWGEGCGRPNRPGVYTRVPAYVNWIRRHI-----TASGGSESGYPRLP
                                     GAWILLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGG---GALRAP
                                                                                                                                                                                                             THHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPV
                                                                                         PYSLREVKVSVVDTETCRRDY-PGPGGSILQPDMLCA---RGPGDACQDDSGGPLVCQVN
                                                                                                                                    POTLOKIKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVD
                                                                                                                                                                                 PSGQPGTSGDTALVELSVPVTLSSRILPVCLPEASDDFCPGIRCWVTGWGYTREGEPLPP
                                                                                                                                                                                                                                                                          MHVCGGSLLSPQWVLTAAHCFSGSLNSSD-YQVHLGELEITLSPHFST---VRQIILHSS
                                                                                                                                                                                                                                                                                                                                                               LGACGLLLLL---AVPGVSLRTLQPGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRLRR 59
                                                                                                                                                                                                                                                                                                                                                                                                          LGTFTSLLLLASTAILNAARIPVPPACGKPQQLN---RVVGGEDSTDSEWPWIVSIQKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRYPSIN_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_012101.
W -> S / TM DOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
M -> V (IN GAMMA-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 569; DB 1;
Pred. No. 5.6e-42;
4; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_012099.
L -> I (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_012098.
S -> T (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_012097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_012100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYPTASE GAMMA LIGHT CHAIN.
TRYPTASE GAMMA HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFF7B06E3C4A962D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IN GAMMA-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                            231
                                                                                                                                    251
                                                                                                                                                                                 175
                                                                                                                                                                                                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

```
MEROPS; S01.025; ...

MGD; MGI:96942; Mcpt6.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001254; Trypsin.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         Hydrolase;
                                                                                                                                                                                                                                                           PIR; A38654; A38654.
PIR; D35646; D35646.
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                             EMBL; M57626; AAA39988.1; -. EMBL; M57625; AAA39987.1; -. EMBL; L31853; AAA39725.1; -. EMBL; X78542; CAA55288.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of at least six distinct mast cell serine proteases,";

Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990).

-I- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.

-I- ALTERNATIVE PRODUCTS: TWO FORMS OF MCPT6 ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SHORT FORM IS PROBABLY AND FUNCTIONAL VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 32-54.
MEDLINE=90222202; PubMed=2326280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=94023807; PubMed=8210998;
Huang R., Abrink M., Gobl A.E., Nilsson
Nilsson K., Hellman L.;
"Expression of a mast cell tryptase in
U-937 and Mono Mac 6.";
Scand. J. Immunol. 38:359-367(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Different mouse mast cell populations express various combinations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen Serafin W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (SHORT FORM). STRAIN-LEADEN X A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang R., Hellman L.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95048582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reynolds D.S., Gurley D.S., Austen K.F., Serafin W.E., "Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by progenitor mast cells and mast cells of the connective tissue subclass.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genes for mast-cell serine protease and their molecular evolution."; Immunogenetics 40:397-414(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LEADEN X A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=91139682; PubMed=1995638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYPSIN FAMILY. TRYPTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chem. 266:3847-3853(1991).
Serine protease; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=7959952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gobl A.E., Nilsson G., Aveskogh M., Larsson L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the human monocytic cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus.
```

SWISS-PROT entry is copyright. It is produced through a collaboration

```
δõ
                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                          TRYT_CANFA
                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                    01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Tryptase precursor (EC 3.4.21.59).
Canis familiaris (Dog).
                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                      P15944;
01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                              TRYT_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                                                                                                                                  176
                                                                                                                                                                                                                                                                                                                                                                                                                                      195
                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                                                                   234 KGTWLQAGVVSWGEGCAQPNKPGIYTRVTYYLDWIHRYV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LLLLASTAILNAARIPVP-PACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
              MAST CELL ACTIVATION.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. STRONGEST TO OTHER TRYPTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LLLLWALSLLASLVYSAPRPA----NQRVGTVGGHEASESKWPWQVSLRFKLNYWIHFCG
                                                  SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
                                                               SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                        DGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEGG-ADVALLELEVPVNVSTHIHPISLPPASETFPPGTSCWVTGWGDIDNDEPLPPPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSLIHPQWVLTAAHCVGPHIKSPQLFRVQLREQYLYYGD-----QLLSLNRIVVHPHYYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQL--GNPGSRSQKVGVAWVEPHPVYSW 134
                                                                                                                                                                                                                                                                                                                                                                                                             LKQVKVPIVENSLCDRKYHTGLYTGDDFPIVHDGMLCAG--NTRRDSCQGDSGGPLVCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                 LQKLKVPIIDSEVCSHLYWRGAGQG----PITED-MLCAGYLEGERDACLGDSGGPLMCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQT 194
                                                                                                                                                                                                                     Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7e splicing.
21
22
31
32
276
75
75
22
122
25
76
76
76
212
249
133
133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
32
75
122
225
225
189
189
133
221
231
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 554; DB 1; Length 276; Pred. No. 9.4e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCMAC...) (POTENTIAL).
GDSGGPLV -> PFCIGDDI (IN SHORT ISOFORM).

MISSING (IN SHORT ISOFORM).

; 525B2C9A04A72200 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE.
MAST CELL PROTEASE 6.
                                                                                                                                                                                                                                                                                                             275
                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
```

```
ŽQ
                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 13, 2002, 08:51:28 Job time: 231 sec
                                                                                                                    δÃ
                                                                                                                                                         밁
                                                                                       Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.7%; Score 546; DB 1; Length 275; Best Local Similarity 40.9%; Pred. No. 4.6e-40; Matches 112; Conservative 46; Mismatches 102; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase;
SIGNAL
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M24664; AAA30854.1; -. PIR; A32410; A32410. HSSP; P20231; 1AAO. MEROPS; S01.143; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                             140 ADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLK 199
                                                                                   200 VPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWL 255
                                                                                                                                                                                                                            256 LAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                 64 IHPQWVLTAAHCVGPNVVCPEEIRVQLREQHL---YYQDHLLPVNRIVMHPNYYTPENG- 119
                                                                                                                                                                                                                                                                                                                       23 LLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG---THHCAGSL 79
                                                                                                                                                                                                                                                                                                                                                                       Serine protease; Signal; Glycoprotein; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 B
211 B
248 B
132 N
30088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION PEPTIDE (BY SIMILARITY).
TRYPTASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
```

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rched:
                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  number of hits satisfying chosen parameters:
     1213.5
660.5
678.5
578.5
578.5
570.5
530.5
539.5
539.5
539.5
539.5
529.5
529.5
529.5
485.5
                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_page:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_virus:*
13: sp_virus:*
14: sp_unclass
15: sp_bacteri:
16: sp_bacteri:
17: sp_archeap
                                                                                                                                                                                                                            Query
Match Length DB
      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              August 13, 2002, 08:47:22; Search time 30.21 Seconds (without alignments) 1815.273 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-040-803-7
1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVVSGAPPALGGGCLGTFTS.....AQGGGALRAPSQGSGAAARS
                                                                                                                                                                                                                                                                                                                                                 sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_plant:*
     297
389
317
320
310
321
310
321
273
799
273
273
273
275
806
 090787
3 09DGR3
3 09DGR3
1 099L44
1 091Z64
096RZ8
1 090Y29
909Y29
1 090Y29
                                                                                                                                                                                                                               Ħ
                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562222
O88781 rattus ratt
O9pvx7 xenopus lae
O9dgr3 xenopus lae
O99144 mus musculu
O91xc4 mus musculu
O9fcr28 homo sapien
O9qyz9 mus musculu
O9smn1 ovis aries
O9dbi0 mus musculu
O9ath0 mus musculu
O9ath4 bos taurus
O42272 xenopus lae
O921n4 mus musculu
O96rz6 homo sapien
O18783 macropus eu
O99ms4 mus musculu
O96rz6 homo sapien
O18783 macropus eu
O99ms4 mus musculu
                                                                                                                                                                                                                              Description
```

4	» ф л ф	4.	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
٥.	. 0		430	30.	432.5	w	433	ω	S	435		437.5	9.	4	445	445.5	445.5	450	452	455.5	462	462.5	463.5	469	472.5	7	475	480
	•	•	25.0		•	•	٠	•	•	٠	•	•	•															
249	2 / 2	261	263	366	767	537	329	265	277	263	581	367	490	810	787	1524	812	334	454	812	492	643	267	624	405	624	624	322
L	3 <u>F</u>	٠ <u>١</u>	11	11	13	4	0	Ų	σı	11	4	11	11	4	տ	13	11	6	6	11	4	6	ы	δ	4	11	11	11
CAMPYO	099670	Q9W7Q4	Q9CR35	070170	Q9DGR2	Q9BYE1	Q9GL10	Q17800	096899	Q9DC86	Q9BYE2	070169	Q920K3	Q15146	Q9VEY6	Q91674	Q91WJ5	046507	046506	Q9R0W3	Q96T73	097506	Q9BK47	Q95ME7	Q96E86	Q9DAT3	Q91Y47	Q920S2
Q9W6KU nococnenia	-	parali		070170 mus musculu	2 xenc	homo			O96899 scolopendra	Q9dc86 mus musculu	omo			Q15146 homo sapien	а	Q91674 xenopus lae			σ	w			Q9bk47 luidia foli		homo	mus	Q91y47 mus musculu	Q920s2 mus musculu

ALIGNMENTS

OR R DDR R D	RR	RESULT O88781 ID OAC ODT ODT ODT ODT ODT OCS R OCS R OCS N OCS N
EMBL; AJ005642; CAA06644.1; HSSP; P00763; LDPO. MEROPS; S01.252; InterPro; IPR001314; Chymotrypsin. InterPro; IPR001314; Trypsin. Pfam; PF00089; trypsin; 1. PRINTS; PR00722; CHYMOTRYBSIN. SMART; SM00020; Tryp_SPC; 1. PROSITE; PS00124; TRYPSIN_DOM; 1. PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1. PROSITE; PS00134; TRYPSIN_SER; 1. HYDROLASE; Protease; Serine protease; Signal. NON_TER	[1] SEQUENCE FROM N.A. STRAIN-FISHER; TISSUE-BRAIN; STRAIN-FISHER; TISSUE-BRAIN; MEDLINE-98389725; PubMed-9722524; Medline-98389725; PubMed-9722524; Davies B.J., Pickard B.S., Steel M., Morris R.G., Lathe R.; "Serine Proteases in Rodent Hippocampus."; J. Biol. Chem. 273:23004-23011(1998)i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.	LT 1 81 81 81 81 81 81 81 81 82 83 84 85 87 88 88 81 81 82 83 84 85 84 85 86 87 87 88 87 88 88 88 88 88

DB 11;

Length

297;

```
RESULT
Q9PVX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC REPRESENTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                             δõ
                                                                                   밁
                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                  DR SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PVX7;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; TTYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN FAMILY.

EMBL; AB018694; BAA84941.1; -.

PHSSP; P00763; IDPO.

MEROPS; S01.UPA; -.

InterPro; IPR001314; Chymotrypsin

InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The expression control of xepsin by non-axial and planar posteriorizing signals in xenopus epidermis." Summitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Amphibia; Batrachia; Anura; Mesobatrachi Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9PVX7
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XEPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIDERMIS SPECIFIC SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 LMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 GVPLPRPQTLQKLKVPIIDPELCKSLYWRGAGQEAITEDMLCAGYLEGKRDACLGDSGGP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 VLPHPRYSRKEGTHADIALVRLERPIQFSERILPICLPDSSVHLPPNTNCWIAGWGSIQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 SIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SPPGL-----TLFILLPSATVSAANIRGSPDCGKPQQLNRVVGGEDSADAQWPWIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 APPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
YLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLP | :: | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : | : : : : | : : : : | : : : : | : : : : : : | : : : : : | : : : : : | : : : : : | : : : : | : : : | : : : : | : : : : | : : : : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGVPVISNRIVGGMDSKRGEWPWQISLSYKSDSICGGSLLTDSWVMTAAHCI-DSLDVS 74
                                                                                                                    ACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMCQVDDHWLLTGIISWGEGCAERNRPGVYTSLLAHRPWVQRIVQGVQLRGRLADSG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222;
                                                                                                                                                                                                        131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                               Protease; Serine protease. 389 AA; 42375 MW; B31FB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.6%;
74.7%;
                                                                                                                                                                                                  38.4%; Score 660.5; DB 13
47.0%; Pred. No. 6.2e-53;
Live 42; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1213.5; DB Pred. No. 3e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                     B31FB4A2F5D1F6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNOWN
                                                                                                                                                                                                                                                                 389;
                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                        6
```

```
RESULT
Q9DGR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                      밁
                                                                                                                                      Ω
                                                                                                                                                                            밁
                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
Š
                                    밁
                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDITINE-20363741; PubMed-10903452;

Yamada K., Takabatake T., Takeshima K.;

"Isolation and characterization of three novel serine
"Isolation and characterization of three novel serine
from Xenopus laevis.";
Gene 252:209-216(200.)
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO K
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DGR3;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00140; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Protease; Serine protease.
Hydrolase; Protease; Serine protease.
SEQUENCE 317 AA; 34413 MW; EEC78A9F45D138FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB038496; BAB08216.1; -. HSSP; P00763; 1DPO. MEROPS; S01.048; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBRYONIC SERINE PROTEASE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9DGR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XESP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193
 241 DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEK
                                                                                                        120
                                                                                                                                           128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 TKVQYYQDWLK---TNVPLIVFSEEGPSV-APSIGPSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 Y-YTVYLGAYQLSAPDNSTVSRGVKSITKHPDFQY-EGSSGDIALIELEKPVTFTPYILP
                                                                                                                                                                            61
                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                1 MGKWLLYVTTLLLEVSPHPSLSNITTAAPPLCGSPVFSSRIVGGTDTRQGAWPWQVSLEF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICLPSQDVQFAAGTMCWVTGWGNIQEGTPLISPKTIQKAEVAIIDSSVCGTMYESSLGYI 192
                                  SEVPLQYPATLQKVMVPIINRDSCEKMYHINSVISETEILIQSDQICAGYQAGQKDGCQG
                                                                                                      SEFNGP-----GTSGDIALLKLSSPIKFTEYILPICLPASPVTFSSGTECWITGWGQTG 173
                                                                                                                                                                                                                                                                                LGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQGSGAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDFSFIQEDMVCAGYKEGRIDACQGDSGGPLVCNVNNVWLQLGIVSWGYGCAEPNRPGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P----ITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQG 219
                                                                    DGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGA----GQGPITEDMLCAGYLEGERDACLG 240
                                                                                                                                        PH---PVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQ 184
                                                                                                                                                                            NGSHICGGSIISDQWILTATHCI-EHPDLPSGCGVRLGAYQLYVKNPHEMTVKVDIIYIN 119
                                                                                                                                                                                                             NGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQL--GNPGSRSQKVGVAWVE 127
                                                                                                                                                                                                                                                                                                                      116;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus.
                                                                                                                                                                                                                                                                                                                                       35.1%;
                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                     Score 603; DB
Pred. No. 1e-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317
                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                        103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                       Length 317;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease
                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes
                                                                                                                                                                                                                                                                                                                        Gaps
```

밁

234

280

```
RN OCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q99L44
                                                                В
                                                                                          Qy
                                                                                                                               В
                                                                                                                                                            Q
                                                                                                                                                                                              망
                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                             DЬ
 В
                           Qy
                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPG; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 339 AA; 36216 MW; BC2DE88BC057,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99L44;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Cast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC003851; AAH03851.1; EMBL; AF378086; AAL06320.1; EMBL; AF378085; AAL06319.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2001) to the -1- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Verghese G.M., Caughey G.H.;
"Molecular cloning and characterization of mouse prostasin, a type membrane associated serine protease of the gamma-tryptase/prostasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99L44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.158; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
 241
                                  245
                                                                181
                                                                                                                                 122
                                                                                                                                                                 128
                                                                                                                                                                                                  64
                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPSIN FAMILY
                                                                                                                               THSSYR-EEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSV
                                                                                                                                                PHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGV 187
                                                                                                                                                                                                               KNGTHHCAGSLLTSRWVITAAHCF-KDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVE 127
PLSCPMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHVAELQPR 291
                              PLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLR 295
                                                               SLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGGKDACQGDSGG
                                                                                           PLPHPQTLQKLKVPIIDSEVCSHLY-WRGAGQGP--ITEDMLCAGYLEGERDACLGDSGG
                                                                                                                                                                                              YDGNHVCGGSLVSNKWVVSAAHCFPREHSREAY - - EVKLGAHQLDSYSNDTVVHTVAQII 121
                                                                                                                                                                                                                                                             LGLGQLEAVTILLLLG--LLQSGIRADGTEASCGAVIQ-PRITGGGSAKPGQWPWQVSIT 63
                                                                                                                                                                                                                                                                                              LGGGCLGTFTSLLLLASTAILNAARIP-VPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ 68
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luvs.
                                                                                                                                                                                                                                                                                                                            33.6%; score 578.5; DB 11; Length 339; 43.0%; Pred. No. 2e-45; Vative 46; Mismatches 109; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO PEPTIDASE FAMILY S1; ALSO KNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              BC2DE88BC057AF10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALSO KNOWN
                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AS
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                              180
                                                                                                                                                                                                                                                                                                                              8
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρ
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                           맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                           01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91XC4
Q91XC4;
                                                                                                                                                                        Protease.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TREMBLREL 19, Last annotation updat
SIMILAR TO DISTAL INTESTINAL SERINE PROTEASE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
                                    "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001).
                                                                                             SEQUENCE FROM N.A.

MEDLINE=21096910; PubMed=11157797;

Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,

Pufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint
                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HS TRANSMEMBRANE TRYPTASE, GENE NAME TMT, AF175522_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010970; AAH10970.1; -.
SEQUENCE
                                                                                  Higgs D.R.;
                                                                                                                                                                                                                                                                                                     Q96RZ8;
                                                                                                                                                                                                                                                                                                                     Q96RZ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia;
Transmembrane.
SEQUENCE 321
                         EMBL; AE006466; AAK61269.1; -.
                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                       254 WLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 ACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LLLLASTAILNAARIPV-PPACGKPQQLNRVVGGEDSTDSEWPWIVS--IQKNGTHHCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LLLL---QILTRARGDILPSVCGHSRDAGKIVGGQDALEGQWPWQVSLWITEDG-HICGG
                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAVPLLDSEDCEKMYHTQGSSLSGERIIQSDMLCAGYVEGQKDSCQGDSGGPLVCSINSS
                                                                                                                                                                                                                                                                                                                                                                                           WTQVGITSWGIGCARPYRPGVYTRVPTYVDWIQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSGDIALVQLDTPLRPSQ-FTPVCLPAAQTPLTPGTVCWVTGWGATQE---RDMASVLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKVPIIDSEVCSHLY-WRG---AGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLIHEVWVLTAAHCFRRSLN-PSFYHVKVGGLTLSLLEPHSTLVAVRNIFVHPTYLWADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33707 MW;
33829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2%; Score 571; DB 11;
1%; Pred. No. 8.9e-45;
50; Mismatches 93
W.
                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FA126747DEAEOAB6 CRC64;
FFF5089EDC4FC73D CRC64;
                                                                                                                                                                                                                                                                                                                      321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                             276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
```

9

```
RESULT POPOZZO POPOZ POP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
B
                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 123;
                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.042; ...
MGD; MGI:1353645; Disp.
MGD; MGI:1353645; Disp.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ243866; CAB56465.1; HSSP; P00763; IDPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1490:131-136(2000)
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=20246299; PubMed=10786627; Shaw-Smith C.J., Coffey A.J., Leve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISP OR DISP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TremBLrel. 19, Last a DISTAL INTESTINAL SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9QYZ9;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9QYZ9
                                                                                                                                                                                                                                                                                             Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walters J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of a novel murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
   10
                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRYPSIN FAMILY
                                 LLLLASTAILNAARIPV-PPACGKPQQLNRVVGGEDSTDSEWPWIVS--IQKNGTHHCAG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGG----GALRAP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYSLREVKVSVVDTETCRRDY-PGPGGSILQPDMLCA---RGPGDACQDDSGGPLVCQVN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSGQPGTSGDIALVELSVPVTLSSRILPVCLPEASDDFCPGIRCWVTGWGYTREGEPLPP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHVCGGSLLSPQWVLTAAHCFSGSLNSSD-YQVHLGELEITLSPHFST----VRQIILHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGACGLLLLL----AVPGVSLRTLQPGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRLRR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGTFTSLLLLASTAILNAARIPVPPACGKPQQLN---RVVGGEDSTDSEWPWIVSIQKNG 71
LLLL---QILTRARGDILPSYCGHSRDAGKIVGGQDALEGQWPWQVSLWITEDG-HICGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAWVQAGIVSWGEGCGRPNRPGVYTRVPAYVNWIRRHI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTLOKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVD 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                            PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                     Protease; Serine protease.
310 AA; 33701 MW; F828EC7F6D25303F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.1%;
                                                                                                                                                32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.J., Leversha M., Freeman T.C., Bentley D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Mismatches 108;
                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 570; DB 4; Length 321; Pred. No. 1.2e-44;
                                                                                                                 Score 564; DB 1
Pred. No. 4e-44;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310
                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae;
                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serine protease
                                                                                                                                                                           Length 310;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TASGGSESGYPRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae;
                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                    9;
```

```
멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
B
                            Qγ
                                                              뭥
                                                                                           QΥ
                                                                                                                              밁
                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XSM1 PRELIMINARY; PRT; 273 AA.

Q9XSM1;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRYPTASE (EC 3.4.21.59).

Qvis arises (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pemberton A.D., McAleese S.M., Huntley J.F., Collie D.D.S., Scudamore C.L., McEuen A.R., Walls A.F., Miller H.R.P.; Scudamore C.L., McEuen B.R., Walls A.F., Miller H.R.P.; CDNA sequence of two sheep mast cell tryptases and the differential expression of tryptase and sheep mast cell proteinase-1 in lung, dermis and gastrointestinal tract."; Clin. Exp. Allergy 30:818-883(2000).
                                                                                                                                                                                                                                                                                                                         PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00134; TRYPSIN_HIS; PR0SITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y18223; CAB41988.1; -. HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                            Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.015; -.
InterPro; IPR001314; Chymotrypsin
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20308142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Caprinae; Ovis.
                                138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                60
                                                                                                                                                                                                               Local
                                                                                              78
                                                                                                                                                            21 LLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ----KNGTHHCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN FAMILY
G-ADIALLQLEEPVSISCHVRPVTLPPASETFPPGSQCWVTGWGNVDNGRPLPPPYPLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKVPIIDSEVCSHLY-WRG---AGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SILTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEG
                              ACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQK 197
                                                                                SLITSRWVITAAHCFKDNLNKFYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEG
                                                                                                                                LHLLALLLLSL--VSAAPGPGQALQRSGIIGGKEAPGSRWPWQVSLRVRDQYWRHQCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTQVGITSWGIGCARPYRPGVYTRVPTYVDWIQRIL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAVPLIDSEDCEKMYHTQGSSLSGERIIQSDMLCAGYVEGHIDSCQGDSGGPLVCSINSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSGDIALVQLDTPLRPSQ-FTPVCLPAAQTPLTPGTVCWVTGWGATQE----RDMASVLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLIHEVWVLTAAHCFRRSLN-PSFYHVKVGGLTLSLLEPHSTLVAVRNIFVHPTYLWADA 124
                                                                SLIHPQWVLTAAHCIGPELQEPSDFRVQLREQHL---YYQDRLLPISRVIPHPHYYMVEN
                                                                                                                                                                                                113;
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                             273 AA;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10848900;
                                                                                                                                                                                                               32.5%;
                                                                                                                                                                                                                                                                             30156 MW;
                                                                                                                                                                                                53;
                                                                                                                                                                                                               Score 559.5; DB 6
Pred. No. 8.8e-44;
                                                                                                                                                                                                                                                                                              TRYPTASE
                                                                                                                                                                                                                                                                                                                                            UNKNOWN_1
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                               88A19DC779053898 CRC64;
                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pecora; Bovoidea;
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                 273;
                                                                                                                                                                                                 15;
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137
                                                                                                                                 59
   175
                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
```

6,

```
R SMART; SM00042; CUB; 1.

R SMART; SM00192; LDLa; 3.

R SMART; SM00192; Tryp_SPc; 1.

PROSITE; PS01180; CUB; 1.

DR PROSITE; PS50068; LDLRA_2; 3.

DR PROSITE; PS50240; TRYPSIN_HOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR Glycoprotein; Hydrolase; Serine protease.

Glycoprotein; Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Fleischmann W., Gojobori T., Bono H., Kasukawa T., Saito R., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pessole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sukynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Hayashinaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01BT60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 1 CUB DOMAIN. EMBL; AK004939; BAB23684.1; -- HSSP; P00763; 1DPO. MGD; MGI:1919003; 1300008A22Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                           PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
|Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
|Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1300008A22RIK PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1300008A22RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DBI0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ω9DВI0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 VKVPIVENSVCDWKYHSGLSTDYSVPIVQEDNLCAG--DGGRDSCQGDSGGPLVCKVNGT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 WILAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 LKVPIIDSEVCSHLYWRGAGQG----PIT-EDMLCAGYLEGERDACLGDSGGPLMCQVDGA 253
                                                                                                                                                                                                                                                                                                         PF00057; ldl_recept_a; 3. PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLQAGVVSWGDGCANPDYPGVYTRITSYLDWIHQYV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799 AA.
```

Query Match

31.2%;

Score 537;

DB 11;

Length 799;

```
δõ
                                               밁
                                                                              QΥ
                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                  Matches 103;
                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50241; TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q29464 PRELIMINARY; PRT; 237 AA. Q29464; Q1-10V-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) TRYPTASE (EC 3.4.21.59) (FRAGMENT).
                                                                                                                                                                                                        SEQUENCE
116 SRSQKVGVAWVEPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTH 174
                                                                                                                                                                                                                         Hydrolase; Serine protease.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X94982; CAA64438.1; -. HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cDNA cloning and primary structure of tryptase from bovine mast cells and evidence of the expression of bovine pancreatic trypsin inhibitor mRNA in the same cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ascoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LIVER CAPSULE;
MEDLINE=96203914; PubMed=8620861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pallaoro M., Gambacurta A., Fiorucci L., Mignogna G., Barra D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                59 SEWPWIVSI---QKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPG 115
                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786 RVTRVINWIQQVL 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 726 RYQVSPRMLCAGYRKGKKDACQGDSGGPLVCREPSGRWFLAGLVSWGLGCGRPNFFGVYT 785
                                  2 SQWPWQVSLRVSRRYWRHHCGGSLIHPQWVLTAAHCVGPEVHGPSYFRVQLREQHL---Y 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 SLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 OGPITEDMLCAGYLEGERDACLGDSGGPLMC-QVDGAWLLAGIISWGBGCAERNRPGVYI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       673 RPVCLPARSHFFEPGQHCWITGWGAQREGGPVSN--TLQKVDVQLVPQDLCSEAY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 LPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 KLWTVFLGKMRQNSRWPGEVSFKVSRLFLHP---YHEEDSHDYDVALLQLDHPVVYSATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 YLFSVLLGAWQLGN--PGSRSQKVGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    556 CGLQGLSSRIVGGTVSSEGEWPWQASLQIRGRHICGGALIADRWVITAAHCFQEDSMASP 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 CGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCF-KDNLNKP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103;
                                                                                                                                                                                                  237 AA; 26550 MW; EA537A75294EFFBA CRC64;
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237:100-105(1996)
                                                                                                        31.2%; Score 536; DB 6; Length 237; 42.6%; Pred. No. 1.1e-41; tive 48; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.1e-41;
4: Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                672
                                                                                                        7;
```

Search completed: August 13, 2002, 08:51:08 time: 226 sec

,",

```
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MInimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein -
                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of hits satisfying chosen parameters:
               581.5
554.5
531.5
531.5
530.5
530.5
530.5
530.5
530.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
529.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       August 13, 2002, 08:45:12; Search time 13.05 Seconds (without alignments) 593.327 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-040-803-7
1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVVSGAPPALGGGCLGTFTS.....AQGGGALRAPSQGSGAAARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/ABCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
             DB
    US-08-944-483-66
US-08-978-404B-21
US-08-978-404B-27
US-08-978-404B-15
US-08-978-404B-16
US-09-016-366A-21
US-08-978-404B-16
US-08-978-404B-14
US-08-978-404B-14
US-08-978-404B-3
US-08-944-483-63
US-09-079-970A-5
US-09-079-970A-6
US-08-944-483-63
US-08-944-483-63
US-08-944-483-63
US-08-944-83-64
US-08-944-83-63
US-08-944-83-64
US-08-948-518-64
US-09-008-518-046-2
US-09-008-518-046-2
US-09-008-518-046-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compugen Ltd
Sequence 66, Appli
Sequence 15, Appli
Sequence 21, Appli
Sequence 3, Appli
Sequence 21, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 6, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
```

4 O	4 4	. A	42	41	40	39	38	37	36	ω	34	33	32	31	30	29	28
443.5	443.5	445.5	446	446	446	446	446	446	446	446	446	446	447	449	449	453	453
25.8	0 0	25.9	25.9	25.9	25.9	25.9	25.9	25.9	25.9	25.9	25.9	25.9	26.0	26.1	26.1	26.3	26.3
86/	86/	256	810	810	810	810	791	791	791	790	790	546	814	791	791	283	283
ď	- ۱	N	6	4	ب	Н	4	N	N	2	٢	6	ب	ω	۰	4	ω
PCT-US94-00616-2	US-08-200-900A-2	US-09-027-337-3	5200340-8	US-09-086-514-1	US-08-147-000B-29	US-07-854-603-2	US-09-132-154-1	US-08-832-087B-1	US-09-131-995-1	US-08-469-658-54	US-08-469-486-54	5200340-6	US-08-750-711-1	US-08-851-350-1	US-08-643-219-1	US-09-478-957-1	US-08-807-151-1
Sequence 2, Appli	Sequence 2, Appli	Sequence 3, Appli	Patent No. 5200340		29	2	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 54, Appl	Sequence 54, Appl	Patent No. 5200340	Sequence 1, Appli				

ALIGNMENTS

RESULT 1 US-08-944-483-66

; MOLECULE TYPE: NO. US-08-944-483-66

6232456e

```
QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-016-366A-15; Sequence 15, Application US/09016366A; Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stevens, Richard L. APPLICANT: Huang, Chifu
                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 PNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 PPNTHCWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGA-GQGP--ITEDML 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 QLGNPGSRSQKVGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 CAGYLEGERDACLGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 KIVQGVQLR 295
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 SKVTELQPR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 VVGGEDSTDSEWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ITGGSSAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE-AYEVKLGAH 59
                                                                                                                                                                                               REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
                                                                                                                                                                                                                NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                  STRANDEDNESS: single
                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLDSYSEDAKVSTLKDIIPHPSY-LQEGSQGDIALLQLSRPITFSRYIRPICLPAANASF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boston
                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                              617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%;
                                                                                                                                                                                                                                                                                          60/037,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 581.5; DB 4;
Pred. No. 6.5e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
```

```
4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-016-366A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-978-404B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
US-08-978-404B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                  TOPOLOGY: 1
MOLECULE TYPE:
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
                                                                                                                                                                      REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 LKQVKVPIVENSLCDRKYHTGLYTGDDFPIVHDGMLCAG--NTRRDSCQGDSGGPLVCKV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 KEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 KGTWLQAGVVSWGEGCAQPNKPGIYTRVTYYLDWIHRYV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 DGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LLLLASTAILNAARIPVP-PACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 GSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQL--GNPGSRSQKVGVAWVEPHPVYSW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: WOLL, --
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 25-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                STRANDEDNESS:
                                                                   TYPE: amino acid
                                                                                                                                                                                                                                           NAME:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                    TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQKLKVPIIDSEVCSHLYWRGAGQG---PITED-MLCAGYLEGERDACLGDSGGPLMCQV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEGG-ADVALLELEVPVNVSTHIHPISLPPASETFPPGTSCWVTGWGDIDNDEPLPPPYP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSLIHPQWVLTAAHCVGPHIKSPQLFRVQLREQYLYYGD-----QLLSLNRIVVHPHYYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
                                                                                                                                                                                                                                          Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stevens, Richard L.
VENTION: MAST CELL PROTEASE THAT CLEAVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                  linear
                                                                                                                                                                                                                                                                                                                                               25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                  No. 5968782e
                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                    Dos
                                                                                                                                                                                                                                                                                                                                                                 US/08/978,404B
                                                                                                                                                                                                                                                                                                60/032,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 554; DB 2; pred. No. 3.2e-47;
                                                                                                                                                                                                             в0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

```
; MOLECULE TYPE: US-08-978-404B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-978-404B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 116; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08978404B Patent No. 5968782
                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDATE OF STREET: OF BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 DGAWLLAGIISWGEGCAERNRPGYYISLSAHRSWYEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 LQKLKVPIIDSEVCSHLYWRGAGQG---PITED-MLCAGYLEGERDACLGDSGGPLMCQV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AEGG-ADVALLELEVPVNVSTHIHPISLPPASETFPPGTSCWVTGWGDIDNDEPLPPPYP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 LKQVKVPIVENSLCDRKYHTGLYTGDDFPIVHDGMLCAG--NTRRDSCQGDSGGPLVCKV 233
                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
                                                  STRANDEDNESS:
                                                                                                                                                                                                                             REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/978,404B FILING DATE: 25-NOV-97 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                      TELEX:
                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 GSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQL--GNPGSRSQKVGVAWVEPHPVYSW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LLLLASTAILNAARIPVP-PACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCA 76
                                                                                           LENGTH:
                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                       NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGTWLOAGVVSWGEGCAOPNKPGIYTRVTYYLDWIHRYV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSLIHPQWVLTAAHCVGPHIKSPQLFRVQLREQYLYYGD-----QLLSLNRIVVHPHYYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLLWALSLLASLVYSAPRPA----NQRVGIVGGHEASESKWPWQVSLRFKLNYWIHFCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: U.S.A.
02210-2211
                                                                                                                                                                                                                                                                   Plumer, Elizabeth R.
                                                                         amino acid
                                                                                         274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 Atlantic Avenue
                                                                                                                                                                        617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stevens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 48; Mismatches
                                  linear
                  No. 5968782e
                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.2%; Score 554; DB 2; Length 276; 41.6%; Pred. No. 3.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAST CELL PROTEASE THAT CLEAVES
                                                                                                                                                                                                                                               36,637
                                                                                                                                                                                                                                 B0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
```

```
ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-008-271A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09008271A Patent No. 6203979
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 40.6%; Matches 117; Conservative '
                                                                                                                                                                          TELEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 DEPLLPPYPLKQVKVPIVENSLCDRKYHTGLYTGDDVPIVQDGMLCAG--NTRSDSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQG---PITED-MLCAGYLEGERDACLGD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 VHPH-YYTVEDG--ADIALLELEIPVNVSTHIHPISLPPASETFPSGTSCWVTGWGDIDS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 VEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 LLLLAST---AILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGT---HH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LLLLALSPLASLVHAAPCPVKQRVG-----IVGGREASESKWPWQVSLRFKFSFWMHF 57
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mohan Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/008,271A FILING DATE: 16-Jan-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBSAtSEQ for Windows Version
CURRENT APPLICATION DATA:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                             TOPOLOGY: 11
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
Hillman, Jenn:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGPLVCKVKGTWLQAGVVSWGEGCAEANRPGIYTRVTYYLDWIHRYV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGSLIHPQWVLTAAHCVGLHIKSPELFRVQL-----REQYLYYADQLLTVNRTV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQ------KVGVAW 125
                                                                                                        LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
                       CLONE:
                                                                                                                                                                                                                                             TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Dr.
                                          LIBRARY: PROSTUT03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guegler, Karl J
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yue, Henry
                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.1e-45; 6; Mismatches 84
                                                                                                                                                                                                                                                                                            PF-0458 US
ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
```

US-09-008-271A-3

```
망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-016-366A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09016366A Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
                                                       TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                     TELEPHONE: 617-720-3500
                                                                                                                                                                                                             APPLICATION NUMBER: 60/037,090 FILING DATE: 05-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS
                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VSNIYLSPR----YLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 GMSQPDPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GGALRAPS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 DSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 GYIKEDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFG
                                                                                                                                                      REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 WDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTR-YF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GCLGTFTSLLLLASTAIL---NAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 NGTHHCAGSLLTSRWVITAAHCFK--DNLNKPYLFSVLLGA------WQLGNPGSRSQK 120
                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGVAWVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSGGPLACNKNGLWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
: 274 amino acids amino acid
                                                                                                                                                                                               Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΜĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                  617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolf,
                                                                                                                                                                                                                                                                                                                  January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.9%;
                                                                                                                                                                            36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Mismatches 115;
                                                                                                                                                            B0801/7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 531.5; DB 4; Pred. No. 6.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; STRANDEDNESS: ; TOPOLOGY: lir US-09-016-366A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-978-404B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08978404B Patent No. 5968782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield & Sacks, P.C.
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 DERLPPFFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 IVHPQFYTAQIG--ADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                 TELEPHONE: 01,
TELEPHONE: 01,
TELEPHONE: 01,
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                          NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-DEC
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 SLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG---THHCA 76 :||||| : |:|| || : : | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                  STRANDEDNESS:
                                                          TYPE:
                                                                       LENGTH:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GSLLTSRWVITAAHC----FKD-----NLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NILLILALPVI--ASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRY: U.S.A.
02210-2211
                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600 Atlantic Avenue
                                                                     274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version
                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                     04-DEC-1996
                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Score 530.5; 39.2%; Pred. No. 6.8
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sod
                                                                                                                                                                                                                                                                                                                                                                            US/08/978,404B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                             в0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8e-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YQDQLLPVSRI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
```

```
US-08-978-404B-16
```

```
US-09-016-366A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-016-366A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09016366A Patent No. 5955431
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/037,090
FILLING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                      TOPOLOGY:
                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 IVHPQFYTAQIG--ADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDN 164
                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 1BM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 SGGPLYCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 DERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                         TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 GSLLTSRWVITAAHC----FKD-----NLNKPYLFSVLLGAWOLGNPGSRSOKVGVAWV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 SLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG---THHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NLLLLALPVL--ASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCG 59
                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MA
                                                                                                                                                                                     275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                  617-720-244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   January 30, 1998
                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.8%; Score 530.5; DB 2; 39.2%; Pred. No. 6.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----YQDQLLPVSRI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 274;
```

```
US-08-978-404B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-978-404B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08978404B Patent No. 5968782
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04 DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7
                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.8%; Score 530.5; DB 2 Best Local Similarity 39.6%; Pred. No. 6.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                MOLECULE TYPE:
                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                            TYPE: amino acid
STRANDEDNESS: single
                             TOPOLOGY:
                                                                                                                                    TELEPHONE: 617-720-2441
                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 DEPLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDMLCAG--NSQRDSCKGD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 IVHPQFYIIQTG--ADIALLELEEPVNISSRVHTVMLPPASETFPPGMPCWVTGWGDVDN 165
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 GSLLTSRWVITAAHCF----KD-----NLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 SLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SLLLLALPVL--ASRAYAAPAPVQALQQAGIVGGQEAPRSKWPWQVSLRVRDRYWMHFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSLIHPQWVLTAAHCLGPDVKDLATLRVQLREQHLY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                           275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stevens, Richard L.
VENTION: MAST CELL PROTEASE THAT CLEAVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                               25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                     DOS
                                                                                                                                                                                                                                                                                                                                                                                                 for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRINOGEN
                                                                                                                                                                                                                                                                                                                                                                  US/08/978,404B
                                                                                                                                                                                                        B0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----YQDQLLPVSRI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

9;

9

```
Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-016-366A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
                                                                              US-09-016-366A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09016366A Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
             Query Match
Best Local Similarity
                                                                                                                                                         INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 DEPLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDMLCAG--NSQRDSCKGD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 IVHPQFVIIQTG--ADIALLELEEPVNISSRVHTVMLPPASETFPPGMPCWVTGWGDVDN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 SGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 30.8%; Score 530.5; DB 2
Local Similarity 39.6%; Pred. No. 6.8e-45;
hes 114; Conservative 50; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 GSILTSRWVITAAHCF----KD-----NLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 SLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQ---KNGTHCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GSLIHPQWVLTAAHCLGPDVKDLATLRVQLREQHLY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SLLLLALPVL--ASRAYAAPAPVQALQQAGIVGGQEAPRSKWPWQVSLRVRDRYWMHFCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                        NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637 REFERENCE/DOCKET NUMBER: BO
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/037,090 FILING DATE: 05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                     TOPOLOGY: li
                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600 Atlantic Avenue
                                                                                                                                                                                                                                                617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                   linear
                                                                                                                       single
  30.8%;
                                                                                                                                                                                                                                                                                                                 B0801/7093
  Score 529.5; DB 2; pred. No. 8.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YQDQLLPVSRI 107
                          Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37; Gaps
```

```
Qy
                                                                                                                                밁
                                                                                                                                                              QΥ
                                                                                                                                                                                                В
                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                   망
                                                                 DЬ
                                                                                                                                                                                                                                                                                                                                  Matches 113; Conservative 52; Mismatches
106 IVHPQEYTAQIG--ADIALLELEEDVNVSSHVHTVTLPDASETEPPGMPCWVTGWGDVDN 163
                                                                 164 DERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAG--NTRRDSCQGD 221
                                                                                               186 GVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGP----ITEDMLCAGYLEGERDACLGD 241
                                                                                                                                                                  127 EPHP-VYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQD 185
                                                                                                                                                                                                                                   77
                                                                                                                                                                                                59 GSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLY------YQDQLLPVSRI 105
                                                                                                                                                                                                                                                                                                  20 SLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNG---THHCA 76
                                                                                                                                                                                                                                                                 GSLLTSRWVITAAHC----FKD-----NLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWV 126
                                                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                              37; Gaps
```

Search completed: August 13, 2002, 08:47:36 Job time: 144 sec

. .

